

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 15, 2006, 20:35:01 ; Search time 188 Seconds  
(without alignments)  
1836.977 Million cell updates/sec

Title: US-10-698-096-17

Perfect score: 3995  
Sequence: 1 MQKNKLKLVKALPSPIDYFN.....VELSRASSRGVINFGPSIK 786

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_21.\*  
1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004s.\*  
9: geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3527	88.3	787	7	ADDD43701
2	3507.5	87.8	787	6	ABBR82565
3	3507.5	87.8	787	7	ADN08758
4	3505	87.7	787	3	AAV59284
5	3505	87.7	787	8	ADG88542
6	3499.5	87.6	787	6	ABBR82567
7	3243.5	81.2	788	7	ADDD43703
8	3243.5	81.2	788	7	ADN08783
9	3239	81.0	788	7	ADN08753
10	3235	81.0	788	7	ADN08762
11	3182.5	79.7	789	2	AAW46862
12	3182.5	79.7	789	2	AAW46862
13	3180.5	79.6	789	2	AAW46863
14	3180.5	79.6	789	2	AAW46863
15	3176.5	79.5	789	2	AAW46867
16	3176.5	79.5	789	2	AAW46867
17	3175.5	79.5	789	2	AAW46867
18	3175.5	79.5	789	2	AAW46867
19	3175.5	79.5	789	2	AAW46867
20	3175.5	79.5	789	2	AAW46867
21	3175.5	79.5	789	2	AAW46867
22	3171.5	79.4	789	2	AAW46867
23	3171.5	79.4	789	2	AAW46867
24	3171.5	79.4	789	2	AAW46867

25	3171.5	79.4	789	8	ADN61600	Adn61600 VIP3A tox
26	3171.5	79.4	789	9	AEA62843	Aea62843 Bacillus
27	3171.5	79.4	789	9	AEA61740	Aea61740 Bacillus
28	3171.5	79.4	809	2	AAW91261	AAW91261 VIP3A(a)
29	3171.5	79.4	809	2	AAW19521	AAW19521 B. cereus
30	3171.5	79.4	809	2	AAW46732	AAW46732 Maize Opt
31	3170.5	79.4	789	2	AAW46860	AAW46860 Bacillus
32	3170.5	79.4	789	2	AAW46868	AAW46868 Bacillus
33	3170.5	79.4	789	2	AAW46869	AAW46869 Bacillus
34	3170.5	79.4	789	2	AAW46871	AAW46871 Bacillus
35	3170.5	79.4	789	2	AAW46872	AAW46872 Bacillus
36	3170.5	79.4	789	2	AAW46873	AAW46873 Bacillus
37	3167.5	79.3	789	2	AAW80320	AAW80320 Bacillus
38	3167.5	79.3	789	2	AAW80321	AAW80321 Bacillus
39	3160	79.1	786	7	ADDD43705	ADDD43705 Bacillus
40	3158.5	79.1	790	2	AAW60215	AAW60215 Bacillus
41	3156.5	79.0	789	2	AAW91244	AAW91244 B. thurin
42	3156.5	79.0	789	2	AAW19515	AAW19515 B. cereus
43	3156.5	79.0	789	2	AAW80321	AAW80321 Bacillus
44	3156.5	79.0	789	2	AAW46726	AAW46726 Native ve
45	3151	78.9	790	2	AAW46872	AAW46872 Bacillus

#### ALIGNMENTS

RESULT 1  
ADD43701  
ID ADD43701 standard; protein; 787 AA.  
XX  
AC ADD43701;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Bacillus thuringiensis insecticidal protein ISP3-1099E.  
XX  
KW Insecticidal; plant insect pest; pesticide.  
XX  
OS Bacillus thuringiensis.  
XX  
PN WO2003080656-A1.  
XX  
PD 02-OCT-2003.  
XX  
PP 20-MAR-2003; 2003WO-EP003068.  
XX  
PR 22-MAR-2002; 2002US-0366276P.  
XX  
PR 06-NOV-2002; 2002US-0423999P.  
XX  
PA (PARB ) BAYER BIOSCIENCE NV.  
XX  
XX Arnaut G, Boets A, De Rudder K, Vanneste S, Van Rie J;  
XX WPI; 2003-876903/81.  
XX DR N-PSDB; ADD43700.  
XX  
PT New insecticidal proteins, useful for controlling plant insect pests, and  
PT for increasing resistance to insect damage compared to control plants.  
XX  
XX Claim 3; SEQ ID NO 2; 81pp; English.  
XX  
XX The present invention relates to Bacillus thuringiensis insecticidal  
XX proteins (ADD43701, ADD43703 and ADD43705) and their coding sequences  
XX (ADD43700, ADD43702 and ADD43704). The insecticidal proteins are  
XX insecticidal against Helicoverpa zea, Heliothis virescens, Ostrinia  
XX nubilalis, Spodoptera frugiperda, Agrotis ipsilon, Pectinophora  
XX gossypiella, Scirphophaga incertulas, and Anticarsia gemmatilis. Sesamia  
XX inferens, Chilo partellus and Anticarsia gemmatilis. The proteins are  
XX useful for controlling plant insect pests, and for increasing resistance  
XX to insect damage compared to control plants.  
XX  
XX Sequence 787 AA;

Query Match	88.3%	Score 3527	DB 7	Length 787
Best Local Similarity	87.5%	Pred. No. 3.7e-208		
Matches 685	Conservative 43	Mismatches 55	Indels 0	Gaps 0

QY	4	NNKLSKVALPSFTIDYNGNGYIGFATGDKIDIMNMTEKMTGGDILTLDELTKNQOOLNLSGK	63
Db	5	NKLNARALPSFTIDYNGNGYIGFATGDKIDIMNMTEKMTGGDILTLDELTKNQOOLNLSGK	64
QY	64	LDGVNGSLNDLLAOGNMLDELTELSEKILKIANEQKRVLDVNTKLDALIMLNTLYLPKITSM	1223
Db	65	LDGVNGSLNDLLAOGNMLDELTELSEKILKIANEQKRVLDVNTKLDALIMLNTLYLPKITSM	1224
QY	124	LSDVWKONVALGQIEEYLSKQLEISDKLDIVINVTNLINSTLREIPAYORIKYVNEKE	1835
Db	125	LSDVWKONVALSQTIEEYLSKQLOEISDKLDIVINVTNLINSTLREIPAYORIKYVNEKE	1836
QY	184	ALTSATETNMLKTQODSSHTDILDELTELTELAKSVTKNDVGDGEFFYNTFHDVMIIGNLF	2434
Db	185	ELTFATETTLTKVYEDGSPADIIDELTELTELAKSVTKNEVDGEFFYNTFHDVWGNLNF	2444
QY	244	GRSALKTASSELLAKENLKTSGSEVGVNVNPLYLTLLQAQAPFLTLTTCRKLGLADIDYT	3030
Db	245	GRSALKTASSELLAKENVKTSGSEVGVNVNPLYLTLLQAQAPFLTLTTCRKLGLADIDYT	3040
QY	304	PIMNEHLNKEKEEFRRNIIPLTSLNTPSNPEYECARSDQKAKIIMEAKPGYALVGPESK	3633
Db	305	SIIMNEHLNKEKEEFRRNIIPLTSLNTPSNPEYECARSDQKAKIIMEAKPGYALVGPESN	3644
QY	364	DSIALVLTQYQAKLKHNYQIDKQSLSEIYVGDIDKLLCPDQSEQMYTYNKLIAFNEEYITK	4233
Db	365	DSMTYLKAAQAKLKODYQVDKQSLSEIYVGDIMKLLCPDQSEQIYYTNNTIAFPREYVITK	4244
QY	424	IAFTKKLNSLRYEVTANFYDSSITGDIIDLKKKIESESEAFSPMLNANDGVYMPICHTSET	4833
Db	425	LFTTKKMSLRKEATRNPFYDSSITGDDMLNKTKYVESSEATSRLSASBDGVYMPGLISET	4844
QY	484	FLTPINGFGLVVDENSRLVTLTCKSYLRELTLLATDLSNKEKTLIVPNEGFIISNIVENGL	5433
Db	485	FLTPINGFGLVVDENSRLVTLTCKSYLREILLATDLSNKEKTLIVPNEGFIISNIVENGL	5444
QY	544	EGENLEPMPKANNKMYVDHTGVNGKRYLYYHEDGEPFQIDGKLKLTREYVQYIVKKG	6033
Db	545	EGENLEPMPKANNKMYIDHTGVNGKRYLYYHEDGEPFQIDGKLKLTREYVQYIVKKG	6044
QY	604	AAIYUKDEKNGDYIYEETNNELEDFOAVTKRPIITGTDSSRVHLIFTSONGEAFGANFI	6633
Db	605	AAIYUKDEKNGDYIYEEINNELEDFOAVTKRPIITGTDSSGVHLIFTSONGEAFGANFI	6644
QY	664	SEIRPSEELLSPELLKSDAMVGSOGTWISGNSLINTNSNNGTPRQMLSESYTYSMNTR	7233
Db	665	SEIRPSEELLSPELLKSDAMVGTQAGAMSGNSLITTYTNGTPRQMLPLESISTYSMNTR	7244
QY	724	VNGFQKVTIRNSREYVFERSYLQFSPSKYSIEKFTTYTNTGTYVELSRASRGVINFQDF	7833
Db	725	ITGFQKVTIRNSREYVLEKNFQQLSPKQDSEKFTTANNTGTYVELSRGTGGGNIIFRDF	7844
QY	784	SIK 786	
Db	785	SIK 787	
RESULT 2			
ABB82565			
ABB82565 standard; protein; 787 AA.			
04-FEB-2003 (first entry)			
B. churingiensis native Vip3B polypeptide.			
Vip3; toxin; insecticide; transgenic; delta-endotoxin; Vip3B.			

**Bacillus thuringiensis.**

PN WO200278437-A2.

PD 10-OCT-2002.

PF 01-APR-2002; 2002WO-US010264.

30-MAR-2001; 2001US-0280025P.

PR 04-DEC-2001; 2001US-0336657P.

PA (SYGN ) SYNGENTA PARTICIPATIONS AG.

PI Miles P, Kramer V, Shen Z, Shotkoski F, Warren GW;

WPI; 2003-040603/03.

XX  
XX  
N 10861, 10867-10877.

PT thuringiensis, useful for controlling insects, e.g., lepidopteran insect,

to highly active against a wide range of insect pests.

Claim 4; Page 56-60; 82pp; English.

CC The invention relates to an isolated Vip3 toxin from *B. thuringiensis*  
CC that is active against insects. The toxins are useful for controlling  
CC that is active against insects. The toxins are useful for controlling

CC insects, where the insect is a lepidopteran insect selected from Ostrinia  
CC nubilalis (European corn borer), Plutella xylostella (diamondback moth),

CC *Spodoptera frugiperda* (tall armyworm), *Agrotis ipsilon* (black cutworm),  
CC *Helicoverpa zea* (corn earworm), *Heliothis virescens* (tobacco budworm), S.  
CC *Helicoverpa zea* (corn earworm), *Heliothis virescens* (tobacco budworm), S.

cc *Helicoverpa armigera* (cotton bollworm). *Manduca sexta* (tobacco hornworm).  
cc *Helicoverpa punctigera* (native budworm),  
cc *exigua* (beet armyworm), *Helicoverpa*

Trichoplusia ni (cabbage looper), Pectinophora gossypiella (pink bollworm), and Cochylis hospes (banded sunflower moth). The

CC polynucleotides encoding the toxins are useful to produce an insect-  
CC resistant transgenic plant. The toxins are useful in combination with Bt  
CC resistant transgenic plant. The toxins are useful in combination with Bt

CC delta-endotoxins to increase pest target range. The present sequence  
CC represents a *B. thuringiensis* Vin3R toxin

XX Sequence 787 AA:  
SO

Query Match 87.8% Score 35075. DB 6. Length 787.

Best Local Similarity 87.3%; Pred. No. 5.9e-207;  
Matches 687; Conservative 46; Mismatches 53; Indels 1; Gaps 1.

09 1 MOKNN-KI SVKAI PSEIDYENCYGEATCTKDIMMT EKTETCCDI ET DETI KNOOI I NE 59

1 MNKONTKI NABAI PSEIDYENCIT YCEATCTKDIMMTEKRTDCNUT ETI DEETI KYOOOTI NE 60

60 TSCSI DOUNGSI NDI I JOCNI DEPI SVETI VT ANEONVAT VDIATVET D A TAT BT VMTU ET 1 1 0

61 TSGKI.DGVNGSI.NDI.TACGNI.NTEFI.SKETI.KTANFONQVY.NDIYADKTY.NAINTMT.YTYI.PY. 120

130 TESTE CHIMICOMINARCI CTEUT ACOT WETONCEW DWTATDTH TUCOM ENTETERAWCORTJENNO: 176

```
db      121  TSMT NDUMKRONVAT CI CTREVI EZOT OBTCTCXY DUTMNTAT TYWCEI EPTETED VODUWATNY 100
```

[illegible][illegible]

**QUESTION**

**ANSWER**

[illegible][illegible][illegible]

70

[illegible]

Qy	420	VITTKAIFPKKUNSLSEYVLANPYDSTGSDI	DLNKKKJESSESAEFSMLNANNOGVPIGT	479
Db	421	VITKTLFPRKUNSLSEYVLANPYDSTGSDI	DLNKTUVESSEAYSTLASDVBVIMPLGI	480
Qy	480	ISEFLFPIINGCGLVYDENSRLVTLTCKSVL	RETLATLPSNBEKLIYEPNPGFINIVE	539
Db	481	ISEFLFPIINGCGLVYDENSRLVTLTCKSVL	RETLATLPSNBEKLIYEPNPGFINIVE	540
Qy	540	NGNLEGENLEPPKANNKNAIYDHTGCVNGT	KVLVYHEDBFSQFIDKCLKTEYVIQYI	599
Db	541	NGNLEGENLEPPKANNKNAIYDHTGCVNGT	KALVYHEDBFSQFIDKCLKSKTEYVIQYI	600
Qy	600	VKGKAIYILKOBKNDDIYIEETNNLEDDQAL	TKRPITIGDSSRVMILPISQNGEAPFG	655
Db	601	VKGKASILLKOBKNDDCIYEDTNNLEDDQAL	TKRSEPIITGDSGVMILPISQNGDEAPFG	660
Qy	660	NFIISIRPSEBLLSPELIKSDAMVWSOGT	WISGNSLINSUNVNGTFPROVLSHESYTVS	719
Db	661	NFIISIRLSEBLLSPELINSAMVWSOGT	WISGNSLTINSUNVNGTFPROVLSHESYTVS	720
Qy	720	MAFNVNGFGKVTIIRNSREVVERSYIQP	SSKATISEKPTTTTNNTGVLVELSRASSRGVIN	779
Db	721	MAFNVNGFAKVTIIRNSREVVERSYIQP	SSKATISEKPTTAANNTGVLVELSRTTSGGAIN	780
Qy	780	FGDPSIK	786	
Db	781	FRNPSIK	787	

RESULT 3  
 ADN08758  
 ID ADN08758 standard; protein; 787 AA.  
 AC  
 XX ADN08758;  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE B. thuringiensis vip3b protein SEQ ID NO:7.  
 XX  
 KW vip3c; toxin; protease inhibitor; lepidopteran; tobacco budworm;  
 XX sunflower head moth; beet armyworm; insect-resistance; maize; vip3B.  
 OS Bacillus thuringiensis.  
 PN MO2003075655-A2.  
 XX  
 PD 18-SEP-2003.  
 XX  
 PK 20-FEB-2003; 2003WO-US004735.  
 XX  
 PR 06-MAR-2002; 2002US-0362250P.  
 XX  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX  
 PI Shen Z, Warren GW, Shokkoski F, Kramer V;  
 XX WPI; 2003-788166/74.  
 DR N-PSDB; ADN08757.  
 XX  
 PT New Vip3 toxin encoded by a nucleic acid from Bacillus thuringiensis,  
 PT useful for controlling lepidopteran insects such as tobacco budworm,  
 PT sunflower head moth or beet armyworm, or for producing an insect-  
 PT resistant transgenic plant.  
 XX  
 PS Example 10; SEQ ID NO 7; 118pp; English.  
 XX  
 CC The invention relates to a novel isolated Vip3 toxin that is active  
 CC against insects. The toxin acts as a protease inhibitor. The Vip3 toxin,  
 CC hybrid toxin and nucleic acid molecules are useful for controlling  
 CC lepidopteran insects such as tobacco budworm, sunflower head moth or beet  
 CC armyworm, for producing an insect-resistant transgenic plant, and  
 CC protecting a maize plant against at least one insect pest. The present  
 CC sequence represents native B. thuringiensis vip3B.

XX	Sequence	787 AA:
SQL	Query Match	87.8%; Score 3507.5; DB 7; Length 787;
	Best Local Similarity	87.3%; Pred. No. 5,9e-207;
	Matches	687; Conservative 46; Mismatches 53; Indels 1; Gaps 1;
QY	1	MOKN-KLSVKAIPSFIDYENGIGPATGIDIMNMI PKTNTGSDTLDEILKNOQLINE 59
DB	1	MNKNTKLNAPALPSFIDYENGIGPATGIDIMNMI PKTNTGSDTLDEILKNOQLINE 60
QY	60	ISGLDGVNGSLINDLLAQGNLDTLSKEILLKIANEOKKLVNDVTKIDALINMNTYLPK 119
DB	61	ISGLKIDGVNSLINDLLIQGNLMTLSKEILLKIANEOKQVINDVNNKNAINTMLHLYLPK 120
QY	120	ITSMILSDVMKONVYALGQIEYLSKOLKEISDKLDIVINNVYLINSTLTETIPAYORIKVN 179
DB	121	ITSMILSDVMKONVYALSIQIEYLSKOLKEISDKLDIVINNVYLINSTLTETIPAYORIKVN 180
QY	180	EKFEALTSATEYNKTKTQDSSHTDILDELTELTELAKSVKKNVDGGEFYLNTHFDVWG 239
DB	181	EKFEFDLTFATETTLAKVKNSSPADILDELTELTELAKSVKKNVDGGEFYLNTHFDVWG 240
QY	240	NNLFGRSALKTASELAKENLKTSGSEVGAVNVELIVTALQAKAPLTLTTCRKLGIAD 299
DB	241	NNLFGRSALKTASELAKENVKTSGSEVGAVNVELIVTALQAKAPLTLTTCRKLGIAD 300
QY	300	IDYTPINNHEHLNKEKEEPRVNIPLTSLNTSPNRYEAKRSDQDAKIIMEAKPGYALVGF 359
DB	301	IDYTPINNHEHLNKEKEEPRVNIPLTSLNTSPNRYAAKSNBPAKIVKEKPGYALVGF 360
QY	360	EISDQSLAVLKVYQAKLKHNYYQIDKDSLSEIYVGDIKLCPCPDSEQMYTNNKAPENEX 419
DB	361	EMSUDSLITVLKAYQAKLKQDYQDKDSLSEIYVGDMKLCPCPDSEQIYTTNNIAPENEX 420
QY	420	VITKIAFTTKKLSLRYEVTANFYDSSGTGIDILNKKKILESSEAEFSMLNANDGYMBIGT 479
DB	421	VITKITFTKKONSLRYEATANFYDSSGTGIDILNKKTVESSEAEFYSLASGTGYMBLGI 480
QY	480	ISEFTFLPPINGFGLVYDENSRLVTLTKKSILRELTILATDLSNKKTKLIVPNGFISNIVE 539
DB	481	ISEFTFLPPINGFGLVYDENSRLVTLTKKSILRELTILATDLSNKKTKLIVPPIGFI SNIVE 540
QY	540	NGNLEGNLTPWKANNNKQAYVDHFGVNGYRKVLVYHDEGEFSOPIGDKLKTREYVLOYI 599
DB	541	NGNLEGNLTPWKANNNKQAYVDHFGVNGYRKVLVYHDEGEFSOPIGDKLKSRTREYVLOYI 600
QY	600	VKGKAAIYILKDEKKAGDIYEETNNLEADFOAVTKRFTTGDSRVLHIFTSQNGEABFGG 659
DB	601	VKGKASITLKDENKGDICITYEDTNGLEDPQITIKSFITGIDSSGVHLIFNSQNGEABFGG 660
QY	660	NFIISIRPSEELLSPELIKSDAMVWGSGTWISGNSLINSNNGTRQMLSLSESYTYS 719
DB	661	NFIISIRLSEBDLLSPELINSAMDAMVWGSGTWISGNSLITINSNNGTRQMLSLSESYTYS 720
QY	720	MNFVNVNGFGKVTIRNSREYVPEKSYLOPSSKTIISEKTTTNTNTGLYVELSPRASSRQVIN 779
DB	721	MNFVNVNGFAPVTVANSREVLPEKSYLPOLSPKDISSEKFTTANNTGLYVELSRFTSGGAIN 780
QY	780	FGDSFSIK 786
DB	781	FRNFSIK 787

RESULT 4	
AAV59284	
ID	AAV59284 standard, protein; 787 AA.
XX	
AC	
XX	AAV59284;
DT	
XX	18-APR-2000 (first entry)
XX	
DE	SNP toxin from B. thuringiensis strain KB59A4-6

```

XX  Bacillus thuringiensis; toxin; endotoxin; pesticide; plant pest;
KM  lepidopterans; cleopterans.
XX
XX  Bacillus thuringiensis.
OS  WO9957282-A2.
PN  11-NOV-1999.
XX  11-NOV-1999.
PD  11-NOV-1999.
XX  11-NOV-1999.
PF  06-MAY-1999; 99WO-US009997.
XX  06-MAY-1999; 98US-00073898.
PR  06-MAY-1998; 98US-00073898.
PA  (MYCO ) MYCOGEN CORP.
XX
XX  Faltelson JS, Schnepf HE, Narva KE, Stockhoff BA, Schmeits J,
PI  Loewer D, Dullum CJ, Muller-Cohn J, Stamp L, Morrill G,
PI  Finstad-Lee S;
XX  WPI; 2000-096811/08.
DR  N-PSDB; AAZ58823.
XX
XX  New polynucleotides encoding pesticidally active proteins, useful for
PT  transforming plants for controlling pests.
XX
XX  Claim 2; Page 100-103; 104pp; English.
XX
XX  The invention relates to novel B. thuringiensis isolates, and genes
CC  encoding pesticidal toxins which are toxic to non-mammalian pests. The
CC  genes are useful in the control of non-mammalian pests and especially
CC  plant pests (e.g. lepidopterans and/or cleopterans). The polynucleotides
CC  are useful for transforming plants for controlling plant pests; for
CC  designing primers and probes useful for the identification and
CC  characterization of genes which encode pesticidal toxins. The present
CC  sequence represents a B.c. SUP toxin
XX
XX  Sequence 787 AA;
SQ

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Query Match 87.7%; Score 3505; DB 3; Length 787;  
 Best Local Similarity 87.1%; Pred. No. 8.4e-207;  
 Matches 682; Conservative 45; Mismatches 56; Indels 0; Gaps 0;

```

QY  4 NNTSLVKAALPSFDYFNGIYGFATGIDIMNMIFKNTGTGDLTLDELTKNOQLNLSISGK 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  5 NTKLNARALPSFDYFNGIYGFATGIDIMNMIFKNTGTGDLTLDELTKNOQLNLSISGK 64
QY  64 LDGVSNGSLNDLIAQGNLDTLSKEILKIANEQNKVLDVNTKDAINMLNTYLPKITSM 123
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  65 LDGVSNGSLNDLIAQGNLDTLSKEILKIANEQNKVLDVNTKDAINMLNTYLPKITSM 124
QY  124 LSDVMKONVYALGOIEYLSKQLEISDKLDVINNVNLINSLTEIPYARIRYVNEKFE 183
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  125 LSDVMKONVYALGOIEYLSKQLEISDKLDVINNVNLINSLTEIPYARIRYVNEKFE 184
QY  184 ALTSATETNKTQDSSTHDILDELTELTELAKSVTKNDVDGEFYLNTFHDVWIGNLNF 243
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  185 ELTFATETTLTKVKKDSSPADILDELTELTELAKSVTKNDVDGEFYLNTFHDVWIGNLNF 244
QY  244 GRALTKTASLTAKEMLKTSGSSEGVANNVNLIVLTALQAAPFLTLTCRKLGLADIDYT 303
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  245 GRALTKTASLTAKEMLKTSGSSEGVANNVNLIVLTALQAAPFLTLTCRKLGLADIDYT 304
QY  304 PINNEHLNKEKEEFNVNLTPTLSNTFSNPYERAKSGDKAKTIMEAKPGVALVGEFISK 363
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  305 PINNEHLNKEKEEFNVNLTPTLSNTFSNPYERAKSGDKAKTIMEAKPGVALVGEFISK 364
QY  364 DSIATVAKTVQAKKENVYQIDKSLSEIVYGDIDKLCPDQSEGYTYTNKTAIPNEVYITK 423
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  365 DSIATVAKTVQAKKENVYQIDKSLSEIVYGDIDKLCPDQSEGYTYTNKTAIPNEVYITK 424
QY  424 IATFKLNSLRVETVNTFVSSGTGDDIDANKKIESSEAESESMANNDGYMIGTITSET 483
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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DB  425 IDFTKKAKTLRYEVTANSYDSSTGEIDLANKKKVSSSEAEYRTL SANNDGYMPLGIVISET 484
QY  484 FLTPINGFGLVWENSLVTLTCKSYRETLATDLSNKKETKILVPNGTISNVENGNL 543
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  485 FLTPINGFGLVWENSLVTLTCKSYRETLATDLSNKKETKILVPNGTISNVENGNL 544
QY  544 EGENLEBPWKANNKNAAYVDHTGTVNGKLVYVHEDGEFSQFIDKLKLTQEVYIQYIVKKG 603
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  545 EGENLEBPWKANNKNAAYVDHTGTVNGKLVYVHEDGEFSQFIDKLKLTQEVYIQYIVKKG 604
QY  604 AAIYLDKQKGDYIYESTNNELEDFQAVYKRFITGTDSSVHLIFTSQNGEBAFGNFI 663
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  605 ASIYLDKQKKNENSIYEEINNDLEGFQVYKRFITGTDSSGHIHIFTSQNGEBAFGNFI 664
QY  664 SEIRPSEELSPELISDAWVSGQTMISGNSLINSNVNCTRONLSLESYSTYSNEN 723
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  665 SEIRTSBELSPELISDAWVSGQTMISGNSLINSNVNCTRONPLSSTYSYNFT 724
QY  724 VNGFGKVTIINSREVVPERSYLQFSSKYISEKFTYTTNNGLVYELSRASSRGVYNGDF 783
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  725 VNGFGKVTIANSREVLPEKSYPOLSPKDISKFTTANNTGLVYELSRSTSGALINRDF 784
QY  784 SIX 786
    |||
DB  785 SIX 787

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RESULT 5  
 ADG88542  
 ID ADG88542 standard; protein; 787 AA.  
 XX  
 AC ADG88542;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE Bacillus thuringiensis strain KB59A4-6 SUP toxin protein.  
 XX  
 XX Pesticide; genetic engineering; resistance; toxin; insecticide;  
 KM plant protectant; gene; ds.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 XX US6603063-B1.  
 PN  
 PD 05-AUG-2003.  
 XX  
 PF 07-MAY-1999; 99US-00307106.  
 XX  
 XX 07-MAY-1999; 99US-00307106.  
 PR  
 XX (MYCO ) MYCOGEN CORP.  
 PA  
 XX Faltelson JS, Schnepf HE, Narva KE, Stockhoff BA, Schmeits J;  
 PI Loewer D, Dullum CJ, Muller-Cohn J, Stamp L, Morrill G;  
 PI Finstad-Lee S;  
 XX  
 DR WPI; 2004-008371/01.  
 DR N-PSDB; ADG88541.  
 XX  
 XX New polynucleotide from Bacillus subtilis, which encodes delta endotoxins  
 PT or pesticide proteins, useful in plant genetic engineering, particularly  
 PT for producing plants that are resistant to lepidopteran or coleopteran  
 pests.  
 XX  
 PS Claim 1; SEQ ID NO 54; stpp; English.  
 XX  
 CC The present invention provides an isolated polynucleotide from Bacillus  
 CC thuringiensis (B.c.) strain KB59A4-6 that encodes an active pesticidal  
 CC SUP toxin protein. The invention is useful in plant genetic engineering  
 CC particularly producing plants that express such gene in order to  
 CC effectively control various insects e.g. boll weevil, black cutworm etc.  
 CC The invention is also useful for conferring resistance in plants against  
 CC lepidopterans or coleopterans. The present sequence is Bacillus



QY	360	EISXDSIAVLKXYQAALKKNNYQDKRSLSEIYVGDIDKLCPQOSEMYTINKIAFPNEY	419
Db	361	EISNDSITVLKXYEAKLKONYQVDKDSLSEVIYGMDKLLCPQOSEIYYTNMIVFPNEY	420
QY	420	VITTKIAFTKKLNSLRYEVTANFYDSSTGDIIDANKKIESSEAEFSMANNNDGVYMPGT	479
Db	421	VITTKIDFTKKMTLRYEVTANFYDSSTGDIIDANKKVESEAEAYRILSANDDGYMPLGV	480
QY	480	ISETFLTPINGGLVVDENSRVLTLCKSYLRRETLATDLSNKEYKLIYPPNGFISNIVE	539
Db	481	ISETFLTPINGFGLQADENSRLLITLCKSYLRRELLATDLSNKEYKLIYPPSGFISNIVE	540
QY	540	NGNLTGEGNIEPWKANNKNAIYVDHTGVNGTKVLYVHDEGFESQFIQDKLKLTEYVIOYI	599
Db	541	NGSIEDNIEPWKANNKNAIYVDHTGVNGTKALYVHDEGFESQFIQDKLKSKEYVIOYI	600
QY	600	VKGAALYIKDEKNGDIYIETTNLEEDPQAVTKRPITGTSSRVHLIFTSQNGEAEFGG	655
Db	601	VKGKASITLKDKNQDCIYEDTNNGLDEDFQTIKSFITGTSSSGVHLIFNSQNGDEAFGE	660
QY	660	NFIIEIRPSEELLSPELIKSDAMVSGQGTWISGNSLAINSNNGTFROMLSIESVETYS	719
Db	661	NFTISIRLSEDLSPELINSDAMVSGQGTWISGNSLITNSNNGTFROMLSIESYSTYS	720
QY	720	MNFNVNGFQKVTIRNSREYVFERSYLOFSKXIYSEKFTTTTNTGTLYVELSRASRSGVIN	779
Db	721	MNFNVNGFAKVTIRNSREVLFEEKNYQQLSPKOISEKFTTANNTGTLYVELSRFTSGAIN	780
QY	780	FGDPSIK 786	
Db	781	FRNFSIK 787	
RESULT 7			
ADD43703			
ID	ADD43703 standard; protein; 788 AA.		
XX	ADD43703;		
XX	15-JAN-2004 (first entry)		
DE	Bacillus thuringiensis insecticidal protein ISP3-327D.		
XX	Insecticidal; plant insect pest; pesticide.		
XX	Bacillus thuringiensis.		
XX	WO2003080656-A1.		
XX	02-OCT-2003.		
XX	20-MAR-2003; 2003WO-BP003066.		
XX	22-MAR-2002; 2002US-0366276P.		
XX	06-NOV-2002; 2002US-0423999P.		
XX	(FARB ) BAYER BIOSCIENCE NV.		
XX	Arnaud G, Boets A, De Rudder K, Vanneste S, Van Rie J;		
XX	WPI; 2003-876903/81.		
XX	N-PSDB; ADD43702.		
XX	New insecticidal proteins, useful for controlling plant insect pests, and		
XX	for increasing resistance to insect damage compared to control plants.		
XX	Claim 1; SEQ ID NO 4; 81bp; English.		
CC	The present invention relates to Bacillus thuringiensis insecticidal		
CC	proteins (ADD43701, ADD43703 and ADD43705) and their coding sequences		
CC	(ADD43700, ADD43702 and ADD43704). The insecticidal proteins are		
CC	insecticidal against Helicoverpa zea, Heliothis virescens, Ostrinia		
CC	nubilalis, Spodoptera frugiperda, Agrotis ipsilon, Pectinophora		

CC *gossypiiella*, *Scirphophaga incertulans*, *Chaphalocrocis medinalis*, *Sesamia*  
CC *inferens*, *Chilo partellus* and *Anticarsia gemmatilis*. The proteins are  
CC useful for controlling plant insect pests, and for increasing resistance  
CC to insect damage compared to control plants.

**SQ** Sequence 788 AA;

Query Match	81.2%	Score 3243.5	DB 7	Length 788
Best Local Similarity	80.9%	Pred. No. 1e-190		
Matches 634; Conservative	65	Mismatches 84	Indels 1	Gaps 1

QY	1	NNKLSVYALPSFIDYENGIGYGAATGKQIMMMIPEKTMNGSLTDELILKNOOLNLSGK	63
Dd	5	NTKLNAAPSPFIDYENGIGYGAATGKQIMMMIPEKTMNGSLTDELILKNOOLNLSGK	64
QY	64	LDGVNGSLNDLLAOGNLDTELSKEILIKLANEQNKYLANDVNRKLDALINMLNTVLPKITSM	123
Dd	65	LDGVNGSLNDLLAOGNLDTELSKEILIKLANEQNKYLANDVNRKLDALINMLHIYLPKITSM	124
QY	124	LSDVNTONTALGLQIEYLSKQLEISDKLDVINNVNLINSTLTTEITPAQRIKYVNEKPE	183
Dd	125	LSDVNTONTALGLQIEYLSKQLEISDKLDIINNVNLINSTLTTEITPAQRIKYVNEKPE	184
QY	184	ALTSATETNLTIKODSSHDIIDELITETTELAKSTKNDVDGFEFEYNTFEDWNIQNNLF	243
Dd	185	ELTFPAETITLVKAKODSPDIDDELITETTELAKSTKNDVDGFEFEYNTFEDWVGNLNF	244
QY	244	GRSALKTASBLIAKENLKTSGSEGVGNVNFVLVTALQAKAFLLTTCRKLLGADIDYT	303
Dd	245	GRSALKTASBLIAKENVKTSGSEGVGNVNFVLVTALQAKAFLLTTCRKLLGADIDYT	304
QY	304	PINMEHLNKRKEEFRNIIPTLSNTPSNPNTEKARGSKDKAKITMEAKPGYALYGEETSK	363
Dd	305	SINMEHLNKRKEEFRVNIIPTLSTNTPSNPNYAKVGSDEDAKMTVEAKPGALYGFEMSN	364
QY	364	DSIAVLKVVYQAKLKHNYQIDKDSLSEIYVGDIIDKLCPDQSEOMYVNTKIAFPVEYVITK	423
Dd	365	DSITVLKVEAKLKQNYQVDKDSLSEYIYGDIDKLCPDQSEQIYVNTNIYFPVEYVITK	424
QY	424	IAETFKLNSLRVEYNTANFYDSSTGDIIDNKKKIBSSSEAFSMLANNDGVYMPIGTISET	483
Dd	425	IDETFKKMLRVEYNTANFYDSSTGEIDNKKKIBSSSEAFRTLSANDGVYMPIGVISET	484
QY	484	FLTPINGFGLVVDENSRVLTTCGYSYLAETLLADLSNKEFKLIVPENGFSNIVENGNL	543
Dd	485	FLTPINGFGLQADENSRLITTCGYSYLRLELLADLSNKEFKLIVPPSGFISNIVENGSI	544
QY	544	EGENTLEPMKANNKNAVVDHTGVTGNSTKVLVYHDEDFEQITGDKLAKTEVYIOIYVKGK	603
Dd	545	EBENLEPMKANNKNAVVDHTGVTGNSTKVLVYHKGQGFQITGDKLAKTEVYIOIYVKGK	604
QY	604	AAIYLVKDEKNGDIYIETINNELEDFOAVTKAPITGETDSSRVHLIFTSQNGEAFAGNFI	663
Dd	605	PSIHLDEKNTGYIYHEDTINNLKQDIQITTKPFTTGIDLKGYVLLILKQNGEAGDGFETI	664
QY	664	SEIRBEELISPELTKSDAMWCSOCTWISGNSLINSNVNCTFRQONSLSEYSITSYNNEN	723
Dd	665	LEIKPAEDLISPELTPNPSNMITTPASISGNKLPINLGTNETPQOSLSNYSITSYSTFT	724
QY	724	VNGFGKVTIRNSREVEVFERYSYLOFSKYSITSEKFTTTNTNTLYEELSRAS-SRGVINFGD	782
Dd	725	ASGPNVYVYRNSREVEVFERSNLMSSTSHISGFTETESNNTLYEELSRSGGGHISFEN	783
QY	783	PSIK 786	
Dd	785	VSIK 788	
RESULT	8		
ADNID	ADN08783	standard; protein; 788 AA.	
XX	ADN08783:		



CC hybrid toxin and nucleic acid molecules are useful for controlling  
CC lepidopteron insects such as tobacco budworm, sunflower head moth or beet  
CC armyworm, for producing an insect-resistant transgenic plant, and  
CC protecting a maize plant against at least one insect pest. The present  
CC sequence represents native B. thuringiensis vip3c.

XX  
SQ Sequence 788 AA;

Query Match 81.1%; Score 3239; DB 7; Length 788;  
Best Local Similarity 80.7%; Pred. No. 1.9e-190;  
Matches 636; Conservative 64; Mismatches 86; Indels 2; Gaps 2;

QY 1 MOKNN-KLSVKALPSFIDYFNGIYGFATGIDIMNMIFKTNNGDITLDELILKNQQLANE 59  
DB 1 MNKNNTKLSSTRALPSFIDYFNGIYGFATGIDIMNMIFKTDGQNLTLDELILKNQQLANE 60  
QY 60 ISGKLDGVNGSLNDLIAQGNLDTLSEIKELIKIANEQNVLDVNNKLDALNTMLHTYLPK 119  
DB 61 ISGKLDGVNGSLNDLIAQGNLDTLSEIKELIKIANEQNVLDVNNKLDALNTMLHTYLPK 120  
QY 120 ITSMUSDVKNQVYALGLQIEYLSKQLEISDKLDVINNVVLIINSTLTETTPAYQRIKYVN 179  
DB 121 ITSMUSDVKNQVYALGLQIEYLSKQLEISDKLDVINNVVLIINSTLTETTPAYQRIKYVN 180  
QY 180 EKFEALTSATEMNLTKQDSSHTDILDELTELTELAKSVTKNDVDFEFLNTFHDVMIG 239  
DB 181 EKFEALTSATEMNLTKQDSSHTDILDELTELTELAKSVTKNDVDFEFLNTFHDVMIG 240  
QY 240 NNLFGRSALKTASELILAKENLTKSGSEVGVNVPFLIVLTALQAKAFLLTTCRKLGLAD 299  
DB 241 NNLFGRSALKTASELILAKENLTKSGSEVGVNVPFLIVLTALQAKAFLLTTCRKLGLAD 300  
QY 300 IDYTPIMNEHLNKEKEEFRVNIILPTLSNTPSNPNYEKARGSDKADAKIMEAKPGYALVGF 359  
DB 301 IDYTPIMNEHLNKEKEEFRVNIILPTLSNTPSNPNYEKARGSDKADAKIMEAKPGYALVGF 360  
QY 360 EISKDSIALVTKYQALQKANYQIDKQSLSTIYVGDIDKLCIPQSEOMYTNKTIAPPNEX 419  
DB 361 EISKDSIALVTKYQALQKANYQIDKQSLSTIYVGDIDKLCIPQSEOMYTNKTIAPPNEX 420  
QY 420 VITKIAFTKLANSLRYEVTANFYDSSGTDILNKKKIESEAFSPMLNNDVVPDICT 479  
DB 421 VITKIAFTKLANSLRYEVTANFYDSSGTDILNKKKIESEAFSPMLNNDVVPDICT 480  
QY 480 ISETFLTPINGFGLVVDENSRLVTLTCKSYLRETLATDLSNKEFKLIYPPNGFISNIYE 539  
DB 481 ISETFLTPINGFGLVVDENSRLVTLTCKSYLRETLATDLSNKEFKLIYPPNGFISNIYE 540  
QY 540 NGNLEGENLEPWKANNKAYVDHTGVNGTKVLVYHEDGEFSQFIDDKLKLTREYVIQYT 599  
DB 541 NGNLEGENLEPWKANNKAYVDHTGVNGTKVLVYHEDGEFSQFIDDKLKLTREYVIQYT 600  
QY 600 VNGKAIYVLKDEKNGDIYEETNNLEDDQAVTKRITGTGDSRVLILPISQNGEARPG 659  
DB 601 VNGKAIYVLKDEKNGDIYEETNNLEDDQAVTKRITGTGDSRVLILPISQNGEARPG 660  
QY 660 NFILISIRSEBELISPELIRKSDAVGSOQTWISGNSININSVNGTFRONLSLESYSTYS 719  
DB 661 NFILISIRSEBELISPELIRKSDAVGSOQTWISGNSININSVNGTFRONLSLESYSTYS 720  
QY 720 NMFNNNGRGKVTIRNSREVVERASYIQFSSKTISEKFTTTNNNTGLVYELSRAS-SRGVY 778  
DB 721 NMFNNNGRGKVTIRNSREVVERASYIQFSSKTISEKFTTTNNNTGLVYELSRAS-SRGVY 779  
QY 779 NFGDFSIX 786  
DB 781 SFENVSIK 788

RESULT 10  
ADN08762  
ID ADN08762 standard; protein; 788 AA.  
XX

AC ADN08762;  
XX 17-JUN-2004 (first entry)  
DT  
XX  
DE B. thuringiensis vip3A-C fusion protein SEQ ID NO:11.  
XX  
XX vip3c; toxin; protease inhibitor; lepidopteron; tobacco budworm;  
KM sunflower head moth; beet armyworm; insect-resistance; maize; vip3A-C.  
XX  
OS Bacillus thuringiensis.  
OS Chimeric.  
XX WO2003075655-A2.  
XX 18-SEP-2003.  
PF 20-FEB-2003; 2003WO-US004735.  
XX 06-MAR-2002; 2002US-0362250P.  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
PA  
PI Shen Z, Warren GW, Shotkoski F, Kramer V;  
XX WPI; 2003-788166/74.  
DR N-PSDB; ADN08761.  
XX  
PT New Vip3 toxin encoded by a nucleic acid from Bacillus thuringiensis,  
PT useful for controlling lepidopteran insects such as tobacco budworm,  
PT sunflower head moth or beet armyworm, or for producing an insect-  
PT resistant transgenic plant.  
XX  
PS Claim 12; SEQ ID NO 11; 118pp; English.  
XX  
CC The invention relates to a novel isolated Vip3 toxin that is active  
CC against insects. The toxin acts as a protease inhibitor. The Vip3 toxin,  
CC hybrid toxin and nucleic acid molecules are useful for controlling  
CC lepidopteron insects such as tobacco budworm, sunflower head moth or beet  
CC armyworm, for producing an insect-resistant transgenic plant, and  
CC protecting a maize plant against at least one insect pest. The present  
CC sequence represents vipA-C, a B. thuringiensis vip3A-vip3C fusion  
CC protein.  
SQ  
SQ Sequence 788 AA;  
Query Match 81.0%; Score 3235; DB 7; Length 788;  
Best Local Similarity 80.5%; Pred. No. 3.3e-190;  
Matches 634; Conservative 64; Mismatches 88; Indels 2; Gaps 2;

QY 1 MOKNN-KLSVKALPSFIDYFNGIYGFATGIDIMNMIFKTNNGDITLDELILKNQQLANE 59  
DB 1 MNKNNTKLSSTRALPSFIDYFNGIYGFATGIDIMNMIFKTDGQNLTLDELILKNQQLANE 60  
QY 60 ISGKLDGVNGSLNDLIAQGNLDTLSEIKELIKIANEQNVLDVNNKLDALNTMLHTYLPK 119  
DB 61 ISGKLDGVNGSLNDLIAQGNLDTLSEIKELIKIANEQNVLDVNNKLDALNTMLHTYLPK 120  
QY 120 ITSMUSDVKNQVYALGLQIEYLSKQLEISDKLDVINNVVLIINSTLTETTPAYQRIKYVN 179  
DB 121 ITSMUSDVKNQVYALGLQIEYLSKQLEISDKLDVINNVVLIINSTLTETTPAYQRIKYVN 180  
QY 180 EKFEALTSATEMNLTKQDSSHTDILDELTELTELAKSVTKNDVDFEFLNTFHDVMIG 239  
DB 181 EKFEALTSATEMNLTKQDSSHTDILDELTELTELAKSVTKNDVDFEFLNTFHDVMIG 240  
QY 240 NNLFGRSALKTASELILAKENLTKSGSEVGVNVPFLIVLTALQAKAFLLTTCRKLGLAD 299  
DB 241 NNLFGRSALKTASELILAKENLTKSGSEVGVNVPFLIVLTALQAKAFLLTTCRKLGLAD 300  
QY 300 IDYTPIMNEHLNKEEFRVNIILPTLSNTPSNPNYEKARGSDKADAKIMEAKPGYALVGF 359  
DB 301 IDYTPIMNEHLNKEEFRVNIILPTLSNTPSNPNYEKARGSDKADAKIMEAKPGYALVGF 360



QY 360 EISKDSIAVLKVTYQAKLKHNYQIDKDSLSIYVGDIDKLCPPDSEQMYTNTKIAFPNEY 419  
CC EISNDSTITVLKYVEAKLKQNYQVDDKDSISEVITYGDMOKLCPDSEQIYYTNNIVFPNEY 420  
Db 361 EISNDSTITVLKYVEAKLKQNYQVDDKDSISEVITYGDMOKLCPDSEQIYYTNNIVFPNEY 420  
QY 420 VITKIATTKLNSLRIVYTANFYDSSGTGDDIDLNKKKIESSEAFESMLNANDGVYMPIGT 479  
Db 421 VITKIDTKKQKTLRYEVTANFYDSSGTGIDLNKKKIESSEAFESMLNANDGVYMPIGV 480  
QY 480 ISEFELTPINGFGLVVDENSRILVTLCYSYRETLATDLSNKKETKLIIVPNGFISNIIVE 539  
Db 481 ISEFELTPINGFGLVVDENSRILVTLCYSYRETLATDLSNKKETKLIIVPNGFISNIIVE 540  
QY 540 NGNLEGENLEBPWKANNKNAAYVDHTGVNGTKVLYVHEDEGFSQPIGDKLAKTEYVYQYI 599  
Db 541 NGSIIEEDNLEBPWKANNKNAAYVDHTGVNGTKVLYVHEDEGFSQPIGDKLAKTEYVYQYI 600  
QY 600 VKGKAALYLKDEKNGDYIYEETNNLEDPQAVTKRPTITGDSRVHLIFTSQGEBAFG 659  
Db 601 VKGKPSIHLKDEKNGDYIYEETNNLEDPQAVTKRPTITGDSRVHLIFTSQGEBAFG 660  
QY 660 NFIISIRPSEBELSPELIKSDAMVSGQWTWISGNSININNVNCTFRONLSIESYSTYS 719  
Db 661 KFTILLETAPADDLSPELINPNSWITTPGASISGNKLPINLGTNGTRQSLNYSYSTYS 720  
QY 720 MNFVNGFGKVTIRNSREVVFERSYLOFSSKYISEKFTTTNNNTGLYVELSRAS-SRGVI 778  
Db 721 ISFPASEPFWNTVYNSRGVLFERSNLSMSTHISGTIKTESNNGLYVELSRASGGGHI 780  
QY 779 NFGDPSIK 786  
Db 781 SFENVSIK 788

RESULT 11  
AAW46862  
ID AAW46862 standard; protein; 789 AA.  
XX AAW46862;  
XX 11-JUN-1998 (first entry)  
DT  
DE Bacillus thuringiensis toxin designated 86BBI(c).  
XX Toxin; lepidopteran pest; control; Agrotis ipsilon; black cutworm;  
KM Heliothis virescens; Helicoverpa zea.  
XX Bacillus thuringiensis.  
OS  
XX WO9800546-A2.  
PN  
XX 08-JAN-1998.  
PD  
XX 01-JUL-1997; 97MO-US011658.  
PF  
XX 01-JUL-1996; 96US-00674002.  
PR  
XX (MYCO) MYCOGEN CORP.  
PA  
XX Schmepef HE, Wicker C, Narva KE, Walz M, Stockhoff BA;  
PI  
XX MPI; 1998-086971/08.  
DR  
XX N-PSDB; AAV16521.  
PT  
XX New isolated Bacillus thuringiensis isolate(s) - used to obtain genes  
PT encoding toxins which are active against lepidopteran pests such as the  
PT Black cutworm.  
PS  
XX Claim 42; Page 117-120; 183pp; English.  
XX  
CC The present sequence represents a Bacillus thuringiensis toxin which is  
CC active against lepidopteran pests. The toxin isolates can be used for the  
CC control of lepidopteran pests such as Agrotis ipsilon (black cutworm),  
CC Heliothis virescens and Helicoverpa zea. PCR primers and probes can be

CC derived from the polynucleotide encoding the toxin and used for the  
CC amplification and detection of other toxin-encoding sequences  
XX  
SQ Sequence 789 AA;  
Query Match 79.7%; Score 3182.5; DB 2; Length 789;  
Best Local Similarity 79.0%; Pred. No. 5.7e-187;  
Matches 624; Conservative 69; Mismatches 92; Indels 5; Gaps 3;  
QY 1 MOKN-KLSYKALPSFIDYNGYIGFATGDKIDMMI FKTNTGSDLTLDLTKNQOLNE 59  
Db 1 MNKNNTKLSRALPSFIDYNGYIGFATGDKIDMMI FKTDTGNTLTDLTKNQOLNE 60  
QY 60 ISGLDGVNGLNDLDAQNLDTLSKEILIKINEOKVLYNDVTKLDATNLMNTYLPK 119  
Db 61 ISGLDGVNGLNDLDAQNLDTLSKEILIKINEOKVLYNDVTKLDATNLMNTYLPK 120  
QY 120 ITSMLSQVKNQVYALGLQIEYLSKQLEISDKLDVINVNLINSTLTETPAYORIKYVN 179  
Db 121 ITSMLSQVKNQVYALGLQIEYLSKQLEISDKLDVINVNLINSTLTETPAYORIKYVN 180  
QY 180 EKFEALTSATETNKTQDSSHYDIDELTELTELAKSVTKNDVGDGEFYLNTFADYWG 239  
Db 181 EKFEALTSATETNKTQDSSHYDIDELTELTELAKSVTKNDVGDGEFYLNTFADYWG 240  
QY 240 NNLFGRSALKTASLAKENLKTSGSEVGVVNFYLTPLQAKAFLLTTCRKLGLAD 299  
Db 241 NNLFGRSALKTASLAKENLKTSGSEVGVVNFYLTPLQAKAFLLTTCRKLGLAD 300  
QY 300 IDYTPINMEHLNKEKEEFVNLPTLSNTPSNPYEVARGSDDXDAKIMEAKPGYALVGF 359  
Db 301 IDYTSINMEHLNKEKEEFVNLPTLSNTPSNPYEVARGSDDXDAKIMEAKPGYALVGF 360  
QY 360 EISKDSIAVLKVTYQAKLKHNYQIDKDSLSIYVGDIDKLCPPDSEQMYTNTKIAFPNEY 419  
Db 361 EISNDSTITVLKYVEAKLKQNYQVDDKDSISEVITYGDMOKLCPDSEQIYYTNNIVFPNEY 420  
QY 420 VITKIATTKLNSLRIVYTANFYDSSGTGDDIDLNKKKIESSEAFESMLNANDGVYMPIGT 479  
Db 421 VITKIDTKKQKTLRYEVTANFYDSSGTGIDLNKKKIESSEAFESMLNANDGVYMPIGV 480  
QY 480 ISEFELTPINGFGLVVDENSRILVTLCYSYRETLATDLSNKKETKLIIVPNGFISNIIVE 539  
Db 481 ISEFELTPINGFGLVVDENSRILVTLCYSYRETLATDLSNKKETKLIIVPNGFISNIIVE 540  
QY 540 NGNLEGENLEBPWKANNKNAAYVDHTGVNGTKVLYVHEDEGFSQPIGDKLAKTEYVYQYI 599  
Db 541 NGSIIEEDNLEBPWKANNKNAAYVDHTGVNGTKVLYVHEDEGFSQPIGDKLAKTEYVYQYI 600  
QY 600 VKGKAALYLKDEKNGDYIYEETNNLEDPQAVTKRPTITGDSRVHLIFTSQGEBAFG 659  
Db 601 VKGKPSIHLKDEKNGDYIYEETNNLEDPQAVTKRPTITGDSRVHLIFTSQGEBAFG 660  
QY 660 NFIISIRPSEBELSPELIKSDAMVSGQWTWISGNSININNVNCTFRONLSIESYSTYS 719  
Db 661 NFIILISPSBELSPELINPNSWITTPGASISGNKLPINLGTNGTRQSLNYSYSTYS 720  
QY 720 MNFVNGFGKVTIRNSREVVFERSYLOFSSKYISEKFTTTNNNTGLYVELSRAS--RG 776  
Db 721 VYFVSQGDANVIRNSREVLFEKRYMS-GAKDVSEMTTPEKDNFYIELSOGNNLYGCP 779  
QY 777 VINRGPFSIK 786  
Db 780 IVHNDVSIK 789

RESULT 12  
AAV24965  
ID AAV24965 standard; protein; 789 AA.  
XX AAV24965;  
XX 09-SEP-1999 (first entry)  
DT

```

XX DE Bacillus thuringiensis toxin 86Bb1 (c).
XX XX Bacillus thuringiensis; toxin; Ostrinia nubilalis; lepidopteran;
XX KM European corn borer; black cutworm.
XX XX Bacillus thuringiensis.
XX OS MO9933991-A2.
XX PN 08-JUL-1999.
XX PD 15-DEC-1998; 98WO-US026585.
XX PF 31-DEC-1997; 97US-00002285.
XX PR (MYCO ) MYCOGEN CORP.
XX PA
XX PI Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;
XX PI Muller-Cohn J;
XX DR MPI; 1999-40513/34.
XX DR N-PSDB; AAX83882.
XX PT Method for control of European corn borer using Bacillus thuringiensis
XX PT toxins.
XX PS Claim 1; Page 121-124; 174pp; English.
XX XX
XX CC A method has been developed for the control of European corn borer
XX CC (Ostrinia nubilalis), comprising contacting the pest with a pesticidal
XX CC amount of a Bacillus thuringiensis toxin. The method is used for the
XX CC control of European corn borer (Ostrinia nubilalis). The method can also
XX CC be used for the control of other non-mammalian pests, particularly black
XX CC cutworm, and other lepidopteran pests. The present sequence represents a
XX CC Bacillus thuringiensis toxin from the present invention
XX SQ
XX
Query Match          79.7%; Score 3182.5; DB 2; Length 789;
Best Local Similarity 79.0%; Pred. No. 5.7e-187;
Matches 624; Conservative 69; Mismatches 92; Indels 5; Gaps 3;

QY 1 MOKNN-KLSVKALPSFIDYFNIGYGFATGKIDIMNMIKTNITGDTLTDELINNOQLNE 59
DB 1 MNKNNTKLTSTRAIPSIDYFNIGYGFATGKIDIMNMIKTNITGDTLTDELINNOQLNE 60
QY 60 ISGKLDGVNGSLNDLTAQGNLTDELTELSEKILKIANEQNKYLANDVTKDAINMLNTYLPK 119
DB 61 ISGKLDGVNGSLNDLTAQGNLTDELTELSEKILKIANEQNKYLANDVTKDAINMLNTYLPK 120
QY 120 ITSMLSDWKQNYALGLOIEYLSKQKEISDKLDVINNVNLINSTLTETTPAYQRIKYVN 179
DB 121 ITSMLSDWKQNYALGLOIEYLSKQKEISDKLDVINNVNLINSTLTETTPAYQRIKYVN 180
QY 180 EKFEALTSATEINLKTKQDSSHTDILDELTELAKSVTKDNDVDFEFTLNTFHDVWG 239
DB 181 EKFEALTSATEINLKTKQDSSHTDILDELTELAKSVTKDNDVDFEFTLNTFHDVWG 240
QY 240 NNLFSGSALKTASSELAKENLKTSGSEGVGNVNFLLVLRLOAKAFLTLTTCCKLGLAD 299
DB 241 NNLFSGSALKTASSELAKENLKTSGSEGVGNVNFLLVLRLOAKAFLTLTTCCKLGLAD 300
QY 300 IDYTPIMNEHLNKEKEFRVNIPLTSLNTFSNPNYKARGSDADAKIMEAKPGYALVGP 359
DB 301 IDYTPIMNEHLNKEKEFRVNIPLTSLNTFSNPNYKARGSDADAKIMEAKPGYALVGP 360
QY 360 EISKDSIALVKYQAKLKNNYQIDKDSLEIYVGDIDKLCPPQSEOMYTNKCIAPNEX 419
DB 361 EMSNDSITVLKYEAQKQNYQVDKDSLEIYVGDIDKLCPPQSEOMYTNKCIAPNEX 420
QY 420 VITTKIAFTKKNLSRLEVTPANPFDSTGDIIDAKKCISSSEAFSLMANNNDGVMPDGT 479
DB 420 VITTKIAFTKKNLSRLEVTPANPFDSTGDIIDAKKCISSSEAFSLMANNNDGVMPDGT 479

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DB 421 VITKIDFTKMKKTLRYEVTPANFYDSSSTGEIDLKKKVESSEAEVRTLSANDGVMPDGV 480
QY 480 ISEFTPLTPINGPGLVVDENSRLVTLCKSYLRETLATLSNKETLIYVPPNFIATVE 539
DB 481 ISEFTPLTPINGPGLVVDENSRLVTLCKSYLRETLATLSNKETLIYVPPNFIATVE 540
QY 540 NGNLAGSENLPEWPKANKNAVVDHTGVNGTKVLYVHEDGFSQFIDKLTAKTEYVLYQY 599
DB 541 NGNLAGSENLPEWPKANKNAVVDHTGVNGTKVLYVHEDGFSQFIDKLTAKTEYVLYQY 600
QY 600 VKGKAIYLKDEKNGCYIYIETNNLEDFQATVTKRFTTGTDSRVLHIFTSONGEAPFG 659
DB 601 VKGKPSIHLKDEKNGCYIYIETNNLEDFQATVTKRFTTGTDSRVLHIFTSONGEAPFG 660
QY 660 NFIISEIRPSEELISPELTKSDAWGSGTWTISGNSLNINSNVNGTFRNLSTESYSTVS 719
DB 661 NFIISEIRPSEELISPELTKSDAWGSGTWTISGNSLNINSNVNGTFRNLSTESYSTVS 720
QY 720 MNEVNGFGKVTIRNSREVFEKSYLQFSKYSIKETTYTNTGTVYELSRAS--RG 776
DB 721 VYFVSAGDANVRIRNSREVFEKRYMS-GAKDVSMTTKFEKDNFYIELSGQNNLYGCP 779
QY 777 VINFGDPSTIK 786
DB 780 IVHFNDVSIX 789

RESULT 13
AAW46863
ID AAW46863 standard; protein; 789 AA.
XX
XX AAW46863;
AC
XX
XX 11-JUN-1998 (first entry)
DT
XX
XX Bacillus thuringiensis toxin designated 86V1(a).
DE
XX
XX Toxin; lepidopteran pest; control; Agrotis ipsilon; black cutworm;
XX Heliothis virescens; Helicoverpa zea.
KM
XX
XX Bacillus thuringiensis.
OS
XX
XX WO9800546-A2.
PN
XX
XX 08-JAN-1998.
PD
XX
XX 01-JUL-1997; 97WO-US011658.
PF
XX
XX 01-JUL-1996; 96US-00674002.
PR
XX
XX (MYCO ) MYCOGEN CORP.
PA
XX
XX Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;
PI
XX
XX MPI; 1998-086971/08.
DR
XX
XX N-PSDB; AAV16522.
DB
XX
XX New isolated Bacillus thuringiensis isolate(s) - used to obtain genes
PT encoding toxins which are active against lepidopteran pests such as the
PT Black cutworm.
XX
XX Claim 42; Page 122-126; 183pp; English.
XX
XX The present sequence represents a Bacillus thuringiensis toxin which is
XX active against lepidopteran pests. The toxin isolates can be used for the
XX control of lepidopteran pests such as Agrotis ipsilon (black cutworm),
XX Heliothis virescens and Helicoverpa zea. PCR primers and probes can be
XX derived from the polynucleotide encoding the toxin and used for the
XX amplification and detection of other toxin-encoding sequences
XX
XX Sequence 789 AA;
SQ
Query Match          79.6%; Score 3180.5; DB 2; Length 789;

```

Best Local Similarity 78.9%; Pred. No. 7.5e-187;  
Matches 623; Conservative 70; Mismatches 92; Indels 5; Gaps 3;

QY 1 MOKNN-KLSYKALPSFIDYNGIYGFATGIDIMNMIFKTNMGDLTLDEILKNOQLNE 59  
DB 1 MOKNNYKLSARALPSFIDYNGIYGFATGIDIMNMIFKTNMGDLTLDEILKNOQLNE 60  
QY 60 ISGKLDGVNGSLNDLLAQGNLDTELSKEILKIANEQNVLDVNTKLDALNMLNTYLPK 119  
DB 61 ISGKLDGVNGSLNDLLAQGNLDTELSKEILKIANEQNVLDVNTKLDALNMLNTYLPK 120  
QY 120 ITSMLSVDMKQNTALGLQIEYLSKQLEISDKLDIVNNTLINSTLREITPAYORIKYVN 179  
DB 121 ITSMLSVDMKQNTALGLQIEYLSKQLEISDKLDIVNNTLINSTLREITPAYORIKYVN 180  
QY 180 EKFEALTSATEMTNKTQDSHTDILDELTELKASVTQNDVDGPEFYANTFHDVWIG 239  
DB 181 EKFEALTSATEMTNKTQDSHTDILDELTELKASVTQNDVDGPEFYANTFHDVWIG 240  
QY 240 NNLFGRSALKTASBELIAKENIKTSGSEVGNVNFILVLTALQAKAFLLTTCCKLLGLAD 299  
DB 241 NNLFGRSALKTASBELIAKENIKTSGSEVGNVNFILVLTALQAKAFLLTTCCKLLGLAD 300  
QY 300 IDYTPIMNEHLNKEKEEFVNILPTLSNFSNPNYEKARGSDKAKIMEAKPGYALVGF 359  
DB 301 IDYTSIMNEHLNKEKEEFVNILPTLSNFSNPNYAKVKGSDBDKAKIMEAKPGYALVGF 360  
QY 360 EISKDSIALVKYQAKLKQYQIDKDSLSIYVGDIDKLCPPDSQEQMTYTNKIAFPNEY 419  
DB 361 EMSNDSITVLKYVAKKQYQIDKDSLSIYVGDIDKLCPPDSQEQMTYTNKIAFPNEY 420  
QY 420 VITKIAFTKGLNSLRYEVANFYDSSTGDDIDLNKKKISSSEAFSMLNANDGVNPIGT 479  
DB 421 VITKIDFTKGLNSLRYEVANFYDSSTGDDIDLNKKKISSSEAFSMLNANDGVNPIGT 480  
QY 480 ISETFLTPINGFGLVNDENSRVLTLCCKSYLRETLATDLSNKEKLIYPPNGFISNIYE 539  
DB 481 ISETFLTPINGFGLVNDENSRVLTLCCKSYLRETLATDLSNKEKLIYPPNGFISNIYE 540  
QY 540 NGNLEGNLEBPWKANNNAAYVDHGTGNGTAVLYVHEDGERSOFIDGKLAKTEYVQYI 599  
DB 541 NGNLEGNLEBPWKANNNAAYVDHGTGNGTAVLYVHEDGERSOFIDGKLAKTEYVQYI 600  
QY 600 VKGKAALYLDKDEKNGDIYEETNNLEDFQAVTRFTGTDSRVHLIFTSONGEBAFG 659  
DB 601 VKGKPSIHLKDENGDIYHEDTNNNLQDYQITRFTGTDBLKGVYILKSQNGDEMGD 660  
QY 660 NFIISEIRPSEBELISPELLISDAVVSQGTWISGNSININSNVNTRFQNLISLSEYSTYS 719  
DB 661 NFIISEIRPSEBELISPELLISDAVVSQGTWISGNSININSNVNTRFQNLISLSEYSTYS 720  
QY 720 MNFRVNGFGKVTIRNSSEVVPERSYLOPSSKYISEKTTTNTNTGLYVEISRASS--RG 776  
DB 721 VYFSVSDDANVVRIRNSREVLFEKGYMS-GAKDVSEMTYREKDNFYIELSQGNLYGCP 779  
QY 777 VINFGDPSIK 786  
DB 780 IVHFYDVSIK 789

## RESULT 14

AAV24966 standard; protein: 789 AA.

AAV24966;

09-SBP-1999 (first entry)

Bacillus thuringiensis toxin 86v1(a).

Bacillus thuringiensis; toxin; Ostrinia nubilalis; lepidopteran;

European corn borer; black cutworm.

OS Bacillus thuringiensis.

XX W09933991-A2.

XX 08-JUL-1999.

PF 15-DEC-1998; 98WO-US026585.

PR 31-DEC-1997; 97US-00002285.

FA (MYCO) MYCOGEN CORP.

PI Schepf HE, Wicker C, Narva KB, Walz M, Stockhoff BA;

PI Muller-Cohn J;

XX WPJ; 1999-405513/34.

DR N-PSDB; AAX83883.

PT Method for control of European corn borer using Bacillus thuringiensis

PS Claim 1, Page 126-129, 17app; English.

CC A method has been developed for the control of European corn borer  
CC (Ostrinia nubilalis), comprising contacting the pest with a pesticidal  
CC amount of a Bacillus thuringiensis toxin. The method is used for the  
CC control of European corn borer (Ostrinia nubilalis). The method can also  
CC be used for the control of other non-mammalian pests, particularly black  
CC cutworm, and other lepidopteran pests. The present sequence represents a  
CC Bacillus thuringiensis toxin from the present invention

XX Sequence 789 AA;

Query Match 79.6%; Score 3180.5; DB 2; Length 789;  
Best Local Similarity 78.9%; Pred. No. 7.5e-187;  
Matches 623; Conservative 70; Mismatches 92; Indels 5; Gaps 3;

QY 1 MOKNN-KLSYKALPSFIDYNGIYGFATGIDIMNMIFKTNMGDLTLDEILKNOQLNE 59  
DB 1 MOKNNYKLSARALPSFIDYNGIYGFATGIDIMNMIFKTNMGDLTLDEILKNOQLNE 60  
QY 60 ISGKLDGVNGSLNDLLAQGNLDTELSKEILKIANEQNVLDVNTKLDALNMLNTYLPK 119  
DB 61 ISGKLDGVNGSLNDLLAQGNLDTELSKEILKIANEQNVLDVNTKLDALNMLNTYLPK 120  
QY 120 ITSMLSVDMKQNTALGLQIEYLSKQLEISDKLDIVNNTLINSTLREITPAYORIKYVN 179  
DB 121 ITSMLSVDMKQNTALGLQIEYLSKQLEISDKLDIVNNTLINSTLREITPAYORIKYVN 180  
QY 180 EKFEALTSATEMTNKTQDSHTDILDELTELKASVTQNDVDGPEFYANTFHDVWIG 239  
DB 181 EKFEALTSATEMTNKTQDSHTDILDELTELKASVTQNDVDGPEFYANTFHDVWIG 240  
QY 240 NNLFGRSALKTASBELIAKENIKTSGSEVGNVNFILVLTALQAKAFLLTTCCKLLGLAD 299  
DB 241 NNLFGRSALKTASBELIAKENIKTSGSEVGNVNFILVLTALQAKAFLLTTCCKLLGLAD 300  
QY 300 IDYTPIMNEHLNKEKEEFVNILPTLSNFSNPNYEKARGSDKAKIMEAKPGYALVGF 359  
DB 301 IDYTSIMNEHLNKEKEEFVNILPTLSNFSNPNYAKVKGSDBDKAKIMEAKPGYALVGF 360  
QY 360 EISKDSIALVKYQAKLKQYQIDKDSLSIYVGDIDKLCPPDSQEQMTYTNKIAFPNEY 419  
DB 361 EMSNDSITVLKYVAKKQYQIDKDSLSIYVGDIDKLCPPDSQEQMTYTNKIAFPNEY 420  
QY 420 VITKIAFTKGLNSLRYEVANFYDSSTGDDIDLNKKKISSSEAFSMLNANDGVNPIGT 479  
DB 421 VITKIDFTKGLNSLRYEVANFYDSSTGDDIDLNKKKISSSEAFSMLNANDGVNPIGT 480  
QY 480 ISETFLTPINGFGLVNDENSRVLTLCCKSYLRETLATDLSNKEKLIYPPNGFISNIYE 539  
DB 481 ISETFLTPINGFGLVNDENSRVLTLCCKSYLRETLATDLSNKEKLIYPPNGFISNIYE 540

QY	540	NONLEENLEPMPANNKRNAYVDHTGVNGTKVLVYHEDGEFSQFIGDKLKTREYVQYI	559		
Db	541	NSISIEDNLEPMPANNKRNAYVDHTGVNGTKALVYHEDGFSQFIGDKLKPRTBYVQYT	6000		
QY	600	VKGKALVYKDEKNGDIYEETNNLEDPQAVTKREITGTDSRVHLIFTSONGEBAFGG	6558		
Db	601	VKGKPSIHLKDENTGVIYHEDTNNLKQYQITIKRFTYTGDLKGVYLILKSQNGDEAMGD	6666		
QY	660	NHIIIRRESEELLSPELIKSDAMWVSQGTWISGNSLINSVNGTFROMLSIESITYS	719		
Db	661	NHIIIEISSEKLLSPELLNTNNVTSTGSHISGNLTLYQGGRGILKQMLQADSFSTYR	7200		
QY	720	NMFNNVGFQKVTIIRNSREYVFEPSYLFQSSKYSIEKPTTNTNGLYVELSRASS--RG	7767		
Db	721	VYFVSYSGDANVRIIRNSREYVFEKGYMS-CAKDVSEMTTYKFEKDNFTYIELSQNNLYGCP	7799		
QY	777	VINFGDPSIK	786		
Db	780	IVHFYDVSIK	789		
RESULT 15					
AAW46867	standard; protein; 789 AA.				
AAW46867;					
DT	11-JUN-1998	(first entry)			
DE	Bacillus thuringiensis toxin designated 2025(a).				
XX					
KM	Toxin; lepidopteran pest; control; Agrotis ipsilon; black cutworm;				
KW	Heliothis virescens; Helicoverpa zea.				
XX					
OS	Bacillus thuringiensis.				
XX					
FH	Key	Location/Qualifiers			
FT	Misc-difference	97			
FT	/note= "encoded by AT"				
XX					
PN	W09800546-A2.				
XX					
PD	08-JAN-1998.				
XX					
PF	01-JUL-1997;	97WO-US011658.			
XX					
PR	01-JUL-1996;	96US-00674002.			
XX					
FA	(MTCO ) MYCOGEN CORP.				
XX					
PI	Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;				
DR	WPI; 1998-086971/08.				
DR	N-ESDB; AAV16526.				
XX					
PT	New isolated Bacillus thuringiensis isolate(s) - used to obtain genes				
PT	encoding toxins which are active against lepidopteran pests such as the				
PT	Black cutworm.				
XX					
PS	Claim 42; Page 139-142; 183pp; English.				
XX					
CC	The present sequence represents a Bacillus thuringiensis toxin which is				
CC	active against lepidopteran pests. The toxin isolates can be used for the				
CC	control of lepidopteran pests such as Agrotis ipsilon (black cutworm),				
CC	Heliothis virescens and Helicoverpa zea. PCR primers and probes can be				
CC	derived from the polynucleotide encoding the toxin and used for the				
CC	amplification and detection of other toxin-encoding sequences				
XX					
Q0	Sequence 789 AA;				

QY	WOKNN-KLSVKLPSFIDYFNGIYGATGKHOMMMI PKTNNGGDI TLBEILKNOQULANE	59
Db	1 MKNKNTKLSARLPSFIDYFNGIYGATGKHOMMMI PKTDGSGNLTJBEILKNOQULANE	60
QY	ISGKLDGVNGSLNDLLAQGNLDTESKEILIKIANEQNKYLANDVTKLDAINIMLNTYLPK	119
Db	61 ISGKLDGVNGSLNDLLAQGNLDTESKEILIKIANEQNKYLANDVTKLDAINIMLNTYLPK	120
QY	ITSMLSDWKQNYVALGLOIEYLSKOLAEISDKLDVANNVNLNSTLTETPAQRIKYNN	179
Db	121 ITSMLSDWKQNYVALSLQIEYLSKOLAEISDKLDVINNVNLNSTLTETPAQRIKYNN	180
QY	EKFBAIATSATENLNTKQDSHFDILDELTELTELAKSVTKNDVDGEBFPLNTHDWMIG	239
Db	181 EKFEELTRATEITTLKAKKQDSSPADILDELTELTELAKSVTKNDVDGEBFPLNTHDWMIG	240
QY	NNLFGRSALKTASSELLIAKENLKTSGSEVGNVNNFLIVTLAQAKFLITTTCKRLGLAD	299
Db	241>NNLFGRSALKTASELIAKENVKTSGSEVGNVNNFLIVTLAQAKFLITTTCKRLGLAD	300
QY	IDYTFIMNHNKKEBEPFVNLTPLTSNFPSPNPKAKGSPDKAKIIMEAKGVALYGF	359
Db	301 IDYTIMNHNKKEBEPFVNLTPLTSNFPSPNPNKAKVGSBDAKIMEAKGVALYGF	360
QY	EISKOSIAVLKYYQAKLKHANYOIDDQDSLSEIYVGIDIKLCPDQSEQMYTNNKIAFEPNEY	419
Db	361 EKSNDOSIYVLKYYEAKLKQNYGVQDQDSLSEIYVIGTDIKLCPDQSEQIYYTNNIIVEPNEY	420
QY	VITTKLAFITKGLNSLREYVTAIFYDSDTGDI DLNKKKIBESSEAFBSMLANNNDGVNPIGT	479
Db	421 VITTKIDFPKKMKTLAEYVTAIFYDSDTGDI DLNKKKVBESSEAFBSYRLSANDGVNMPLG	480
QY	ISFTPLTPINGGLVVDENSRLVLTLTCKSYLRETLTATPLSKETGLIYPNGFISNIYE	539
Db	481 ISETPLTTPINGGLQADGNSRLITLTCKSYLRETLATPLSKETGLIYPPSGFISNIYE	540
QY	NGNLEGENLEPWKANNKQAYVDHTGVNGTKLYLVEHDEBFSGFTGDKULKTEYIYOYI	599
Db	541 NGSIBEDNLEPWKANNKQAYVDHTGVNGTKLYLHKQGGISQFTGDKLKPTEYIYOYI	600
QY	VKGKRALYLBKQKNDYIYEETNNLEDPQAVTKPFTITDSSRYHLITFSQNGEBAFGG	659
Db	601 VKGKRSIHLKQENTYIYHEDTNNMLKQYQITTKRFTTGTDLKGVYLILKSQNGEDBAMGD	660
QY	NFIIEIRPEBELSPELISKDAWAGSOGTWSGSLNINSNVNGGFRONLSIESYSTYS	719
Db	661 NFIILIEIPSEKULSPELINTNNMTSTGSIHSGNTLITLYQSGRGILKONLQDSDSYTR	720
QY	MNFVNGEGKTYTIRNSREVEFSRYLQFSSKYISSEKFTTTTNNGTLYVELSPASS--RG	776
Db	721 VYFVSYGADNARIIRNSREVLFEKRYMS-GAKOVSEMFTEKFEKDNFYIELSGOONNLYGGB	779
QY	VINRGDPSIK 786	
Db	VHFPDVSIK 789	

Search completed: May 15, 2006, 20:39:13  
Job time : 192 secs

Query Match	79.5%;	Score 3176.5;	DB 2;	Length 789;
Best Local Similarity	78.9%;	Pred. No. 1.3e-186;		
Matches 623;	Conservative 69;	Mismatches 93;	Indels 5;	Gaps 3

GenCore version 5.1.8  
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## OM protein - protein search, using sw model

Run on: May 15, 2006, 20:39:31 ; Search time 44 Seconds

(Without alignments) 1718.781 Million cell updates/sec

Title: US-10-698-096-17

Perfect score: 3995  
Sequence: 1 MQKNKLSVKALPSRIDYFN.....VELSRASSRGVINGDPSIK 786Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	238	6.0	2401	2	T28676 rhoptry protein -
2	225	5.6	1252	2	B42771 reticulocyte-bind
3	208.5	5.2	2166	2	G70163 hypothetical prote
4	206	5.2	1447	2	F82909 hypothetical prote
5	203.5	5.1	1315	2	T28679 fibronogen-binding
6	201	5.0	2269	2	T28677 rhoptry protein -
7	199	5.0	3394	2	T18501 hypothetical prote
8	194.5	4.9	2178	2	S55805 alpha-toxin - Clos
9	194	4.9	1227	2	G97033 uncharacterized pr
10	193.5	4.8	1313	2	G82887 hypothetical prote
11	189.5	4.7	1054	2	G82934 hypothetical prote
12	189.5	4.7	1365	2	T30822 lmp1 protein - Myc
13	189	4.7	1127	2	T28317 ORF MSV156 hypoch
14	187.5	4.7	1051	2	T18351 lmp1 protein - Myc
15	187	4.7	1830	2	B82909 conserved hypochet
16	187	4.7	4919	2	T31105 hypothetical prote
17	184.5	4.6	981	2	C82930 p15 protein Uu140
18	184.5	4.6	1385	2	D89824 hypothetical prote
19	184.5	4.6	2022	2	T43214 hypothetical prote
20	183	4.6	2710	2	A37052 coxin A - Clostrid
21	183	4.6	3216	2	C90538 hypothetical prote
22	183	4.6	5005	2	F82884 hypothetical prote
23	183	4.6	6713	2	B89921 hypothetical prote
24	182.5	4.6	2206	2	G71611 vasa-like (mycopla
25	182	4.6	1017	2	D90550 hypothetical prote
26	181.5	4.5	888	2	E82885 hypothetical prote
27	181.5	4.5	4688	2	F82885 hypothetical prote
28	180.5	4.5	1005	2	A64465 hypothetical prote
29	179.5	4.5	624	2	PC6003 surface membrane p

30	179.5	4.5	1247	2	E71616 hypothetical prote
31	179	4.5	1191	2	B97116 chromosome segrega
32	179	4.5	2823	2	E87908 protein T22A.8 li
33	179	4.5	2823	2	T23064 hypothetical prote
34	179	4.5	3102	2	T43291 laminin alpha chain
35	178.5	4.5	1368	2	T18371 probable glucamate
36	178.5	4.5	2244	2	F90563 hypothetical prote
37	178	4.5	1817	2	H71611 probable secreted
38	178	4.5	2364	2	T40884 cytochrome b - Clos
39	177.5	4.4	1939	2	T18372 repeat organelle
40	177	4.4	967	2	S58360 lantibiotic pep b
41	176	4.4	1306	2	T28313 ORF MSV152 probabl
42	175.5	4.4	896	2	A81514 conserved membrane
43	175	4.4	1778	2	A71116 internal protein
44	174.5	4.4	1025	2	C82886 hypothetical prote
45	174	4.4	786	2	T18469 hypothetical prote

## ALIGNMENTS

## RESULT 1

T28676 rhoptry protein - Plasmodium yoelii (fragment)

C.Species: Plasmodium yoelii

C.Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C.Accession: T28676; A45521

R.Sinha, K.A.; Keen, J.K.; Ogum, S.A.; Holder, A.A.

Mol. Biochem. Parasitol. 76, 329-332, 1996

A&gt;Title: Comparison of two members of a multigene family coding for high-molecular mass

A.Reference number: 220507; MUID:97077455; PMID:8920022

A.Accession: T28676

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-2401 &lt;SIN&gt;

A.Cross-references: UNIPROT:Q26216; UNIPARC:UPI0000178647; EMBL:U36927; NID:G1041784; F

R.Keen, J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.

Mol. Biochem. Parasitol. 42, 241-246, 1990

A&gt;Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple c

A.Reference number: A45521; MUID:91101660; PMID:2270106

A.Accession: A45521

A&gt;Status: preliminary

A.Molecule type: DNA

A.Residues: 2260-2401 &lt;KE&gt;

A.Cross-references: UNIPARC:UPI0000178648; GB:M34281

Query Match 6.0%; Score 238; DB 2; Length 2401;

Best Local Similarity 22.0%; Pred. No. 0.0065;

Matches 168; Conservative 106; Mismatches 256; Indels 232; Gaps 37;

QY	16	IDYFNGIYGFATGICQIDINMIFKTNVGGDLTLDLILKQOL-----LNELSGKIDCV-N 68	
QY	51	LDYFNSIG-----KLIN---KVDSDGNIIEENDIDPDISKPKNNFKLLEGELNGVFE 102	
DB		69 GSINDLAQGNLD---TELSKEILKIANEON--KVANDVNTKLD-----AINMAMNT 115	
DB	103	NKANDYKNNKNDQPKDTMKKILIIIIYNNHFKGANDATKLNKNGISQKFINNQKQ 162	
QY	116	YLPKLT-----SMISDVKNON---VALGLQIEYLSKQLEIS 149	
DB	153	KFDKSTYDEKKKGFPSSLELANWEKKLEIITELKKNGEETVQDIDIKIRELIQIK--- 219	
QY	150	DGLDVNNVNLNSTLTITPAQRIKYNVEKFEALTSATETNLKTKQDSSHTDILDLBT 209	
DB	220	---DIIEQKIVNDKLELN---KKIKETEKIEIKAVLKKIEIKEDVNIYD----- 267	
QY	210	ELTELAK-----SVTKNDVDFEFYLYNT-----FHDVMIG-----NNLFGSALKTASBLI 255	
DB	268	---ELAKPPYQITIKYIKKNEIY-NTIKSPDKIYVDDIQLYNEMFSVQESNIEHIE 323	
QY	256	AKENIKTSGSEVGNVNLIVLTALQAKAPL-TLTTCRL-----LGLADIDYTPIMENHL 310	
DB	324	NKTELILTKTKIDVNNYNNIQNMETETVSKHKNIEFNKLSSETLIDIIKYIYGELTNE-L 382	

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Qy 311 NKEKEFRVNIILPTLSNTPSNPYEKARGS--DKQAK-----IIMEAKPGALVVG 358
Db 383 NKTJLDFK-----NKEKGLSNKIDETAKENVOLNPKYSNLTLEIKRY---- 424
Qy 359 T...SKDSIAVLKVYQAKLKNY-----QIDKDS-LSEI-VY 392
Db 425 ---NDQINIDINIKKEAKQNDQFKEHMKTIIPNEMKYQKPSIELKIMKDFLSKVNY 480
Qy 393 GDIDKLLCPDQSQWYNNKIAFPNEVYITTKIAFLKGLNSLREYAT-----ANFYDSS 445
Db 481 NDFPKV-----YKEKVESEN-----KFTELNKKIKTEVSEDEIKKYEKNKFPDS 524
Qy 446 TGDIDILNKKIISSSEAFESMLNANDGYMPTIGTSETFLPINFGLVNDENSLVLT 505
Db 525 KSLINETKKSIEEYQNTLKKVDYIKVCANTNE-----LITGCHNKQTTLK 573
Qy 506 CK-----SYLRET-----LLAID-----LSNKKETKLIVPNGFISNIVENGNLE----- 544
Db 574 DKLQONIKTIKEIWSIDKIYTDKFPENILTDKKTLETFGTGLSNHESNNKELLTYPYD 633
Qy 545 -----GENLEPM-----KANNKAYVDHTGVN-----GTYKLVYHEDGEFSQ 582
Db 634 LKALIGKXKXKMLYKQFNEKEKAVEDIKKKXVDINKIYVSNIEITITYSIVINEDTE--N 691
Qy 583 FIGDKLKLTEYVIQYIVKGAATYLDKKNGDYIEETNNE 624
Db 692 EIGKSIELNNTKVLKVKVANTYINLEIKLKDYPQDQKX 733

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## RESULT 2

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B42771
reticulocyte-binding protein 2 - Plasmodium vivax (fragment)
C:Species: Plasmodium vivax
C>Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Sep-1997
C:Accession: B42771
R:Galinski, M.R.; Medina, C.C.; Ingravallo, P.; Barnwell, J.W.
Cell 69, 1213-1226, 1992
A:Title: A reticulocyte-binding protein complex of Plasmodium vivax merozoites.
A:Reference number: A42771; MUID:92315338; PMID:1617731
A:Accession: B42771
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1252 <GAL>
A:Cross-references: UNIPARC:UPI000017B645; GB:M88098; NID:g160627; PID:g160628
A:Experimental source: strain Belém, merozoites
C:Genetics:
A:Gene: RBP2

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Query Match 5.6%; Score 225; DB 2; Length 1252;
Best Local Similarity 22.0%; Pred. No. 0.01;
Matches 172; Conservative 124; Mismatches 269; Indels 218; Gaps 43;

Qy 3 KNNKLSV---KALPFIYFNGI-----YGPATGIKDINMMIFKNTGGLTLDEI 50
Db 535 KNRKRVDTTKKSIINSTVGFSFLFNNPDLNQDFPKNINDYEN----- 578
Qy 51 LKNOQLNFIISGLDGVNGL-----NDLDAQNLDELSEILKIAN--EONKVLN 100
Db 579 -KMGELIYFBSGLNKISLNLNASENTSDYNSAKTLRLAOKKEKNLNLKSEENAKYLR 637
Qy 101 DVNTKLDALINMLN--TYLPKITSM--SDVMKQNYALGQIEYLSKQLEISDKLDVIN 157
Db 638 DVK-KVESFRFIFNNKESLDKINEMIKKQLVYNEHG--NKQVLENIMELVDE----- 689
Qy 158 NVLINSTLEITPAVQRIYVNEKEPALTSATENLTKYKDS--SHTD-----ILD 206
Db 690 ---NNLSDI-----LKOATGKNEIQKITHSTLKKAKKATILGHVIDISAKYVGIKTP 738
Qy 207 ELTELTEL-----AKSVTKNDV--DGFETLATFHDVIMGNLFGSALKTASE 253
Db 739 ELA-LTELIGDAKLTQAEQLKFKESKNNVVLLETENNSKOT--NELDVHKNI--QDAYKALE 794

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Qy 254 LIA-----KENLKTSGSEVGNVYVFLVL-----TALOAK----- 283
Db 795 ILAHSDEIDTKQKSSKLIEMGNQYVLKVVLINQYKNNKISSIKSGEAVSVKIGVNSKCH 854
Qy 284 AFLTLTKRKLGLADIDITPIANHEHLNKEKEEPRVNIILPTLSNTPSNPYEKARGSDK 343
Db 855 SELSKITE-----SDKSVDNIIALEKQTELQNIIRNSFTQKRTVNSDKLEKIK----- 903
Qy 344 AKIIMEAKPGYALVGFSEISKDSIAVLKVYQAKL-----HNYQDKD-----SLSEL--V 391
Db 904 -----IDFESLKAALTLBGEVALKAASSDNHSHVOSKEPPVNPALSEIKE 950
Qy 392 YGIDKLLCPDQSQWYNNKIAFPNEVYITTKIAFLTK-----LNSLREYANF-- 441
Db 951 ETDIDSL--NYALDELKKGRGTCVSHYKLIKQIVTIEISDDELINTIEGNVAYLAYI 1008
Qy 442 ---YDSSTGDI-----DLNKKKISSF--AEFSMLNANDGYMPTIGTSETFLTPINGFG 492
Db 1009 KQNEEDTVQDVLTLNHEPNTKQVSNHPTPFDKSNKSEBELYKAV--TDSKTIISKLGYI 1067
Qy 493 LVVDENSLVTLTCKSYLRETILATDLSNKKETKLIVPNGFISNIVENGNLEGENLEPMK 552
Db 1068 IEVVENTEMNTIESSAKETIALLY--NELKXKTSL-----NEIYQTSN--EYKLOEMK 1116
Qy 553 ANNKAYVDHTGVNGTKVLYVHEDGEFSQF-----IGDKLKLTEYVIQYIVK 603
Db 1117 -SNADKYID-----VSKIFNTVLDTPQKSNIVTNGSHINNVDKRLKQK---LOELIDAD 1165
Qy 604 AAIYLDKRNKGDYIYE--ETN--NELDPQAVTR--FITGDTSSRVHLIFTSQNGEAF 657
Db 1166 SSFTLESIKKFNESYIHKITNIGLEBLOQTNKSEHDNVAKHKEKIVHLI-----NRVESL 1221
Qy 658 GGN 660
Db 1222 KGD 1224

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## RESULT 3

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G70163
hypothetical protein BB0512 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: G70163
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Jadhava, R.; White
son, D.; Peterson, J.; Kexlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugc,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roderick, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: G70163
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-2166 <KLE>
A:Cross-references: UNIPROT:O51465; UNIPARC:UPI00000574E8; GB:AE001153; GB:AE000783; NID
A:Experimental source: strain B31

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Query Match 5.2%; Score 208.5; DB 2; Length 2166;
Best Local Similarity 21.5%; Pred. No. 0.12;
Matches 184; Conservative 141; Mismatches 330; Indels 201; Gaps 45;

Qy 3 KNNKLSVALPSPF---IDYF---NGIYGPATGIKDINMMIFKNTGGLTLDE-----IL 51
Db 910 KELKFSISLSYLYLEKIDFRNGALYSDSL--IQDINHNNKRELEENLISKFAAVL 968
Qy 52 KQ-QQLNFIISGLDGVNGLNDLDAQNLDELSEILKIANBQNKVANDVNTKLDALIN 110
Db 969 NNSSEFVKEVDSLQDKRTDIASF--QANIDITDSLNVKFE--NDINK--EINGCNNEVI 1022
Qy 111 LMLNTYLPKITSM--SDVMKQNYALGQIEYLSKQLEISDKLDVINAVNLINSTLEITP 170
Db 1023 SNRYGYSNITSSKLENIH--ETENLSRRL--TDRIIDLSKQ--MDENILOKLE 1071

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QY 171 AVORIKYNEKREBALTSATETMLTKYQ--DSSHTDILDELTELTELAKSVTKNDVDGPEF 228
DB 1072 SFVSKYQVKEFE-----LKVLDIDDDGEAKINKLVKEIQYYKSRLEAID----- 1118
QY 229 YLNTF-HDMWIGNNLFSG-----RSALTKASEL---IAKENLKTSSSEVGNVYN-FLI-- 275
DB 1119 YKRITDNDIMQAKERFGEITNELKNNIESKSEFENDLYKRFPLISNFEERSTPLIS 1178
QY 276 --VLTLQAKAFLLTTCRKLGLADIDYTPIMNEHLNKEKEFRVNIPLTISNTSPN 333
DB 1179 EGASIKRBEIKYLTLS-----NDENLQIKISEM-----DON 1210
QY 334 YKANGSDKDAKIIMEAKPGVALVGEISKDAVLKVYQAKLKNYQIDKSLSEIYVG 393
DB 1211 FE-----LIEQR-----SKDILFEFEKELQDKIKDCYGFINSQGEIKAG 1249
QY 394 DIDKL-----LCPDSEQMYTNKIAFPREYVITKIAFTKGLNSLRBYTANFYDSSTD 448
DB 1250 VEENIKNHFVCIKKNYTLIDDIYKYENE-IHKRIDSLSIESFSDISEKMLNDKVSQC 1308
QY 449 I-----DLNKKKIESSE-AEFSMLNANDGVYMPIGTISETFLTPING-----FGLVND- 497
DB 1309 IDKINDPRLKYILEERCNBQMLNENK-IDNKIKALDNLALSOYDLEKRYADYDEF 1367
QY 498 ---NSRLVTLT-CKSYLRETL-----LATDSLNETKLIVPENGFSINIVE 539
DB 1368 SERLSNYATLSEEFKSNKEMIPELESQKMLKULESDLNVEKDVIRLKESYHNVSS 1427
QY 540 NQNLGEGNLEPWKANKKAYVDHTGVNGTKVLYNHEDGEFSQFIDGKLKTEYVIOYI 599
DB 1428 HKLLEEDP-----FKDLK--IRGEELKYSLEN--FTASYNDKQ-MLKYDLSKN 1472
QY 600 VKGKAIIY-----LKDEKNGDYI--YEETNNLEDPQ--AVTKRFTGTDSRV 644
DB 1473 LENKTELQSFPDLBOQKDKDKENFYDLFTKESKKQMOSEIALMETNITGKXDEFV 1532
QY 645 HLIPTSONGEAFGNGFIISIRPSEBELSPELIKSDAWVSGQTWISGNSLINSNVNG 704
DB 1533 DFNKKQSIIDSWFLN-IKMDVQMOE-----KSYSTIEKR--INLAEIGISFEND 1581
QY 705 TFRQULSLESYSTYGMNPNVNGFGKVTIRNSREVVPEKSYLOPSSKYSSEKTTTNNTG 764
DB 1582 IFNVKIGLESFK-----DGF-----EIKAEIIF--SNLOEAKKIEQSVHLDPKQIG 1626
QY 765 LVELSRASSRGVINF 780
DB 1627 ESNLKVLDLEKVDVF 1642

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## RESULT 4

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F82909
hypochemical protein U293 (!imported) - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: F82909
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Casseil, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A:Reference number: A82870
A:Accession: F82909
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1447 <GAA>
A:Cross-references: UNIPARC:UPI00000CIC06; GB:AE002127; GB:AF222894; NID:96899268; PIDN:
A:Experimental source: setovar 3; Biovar 1
C:Genetics:
A:Gene: U293
A:Genetic code: SGC3

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Query Match 5.2%; Score 206; DB 2; Length 1447;
Best Local Similarity 20.9%; Pred. No. 0.092;
Matches 184; Conservative 141; Mismatches 306; Indels 248; Gaps 49;

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QY 29 IKDIM-----NMIFKNTNG-----GDLTLEI-----LKN--QOLNIEISGLDGVNS 70
DB 124 VQDVNNDDHHNMLMKQNTSFSHKSDDLKIKIQLVLPQKNEYQOLVNNLNGIDPKR-V 182
QY 71 LNDLLAQNLDELSEKILKIANEON-----KVIN--DVNTK-----LDAINIMLNTY 116
DB 183 VQNLIVGFAKIIDHQOOLK--NSQNFGLIQKVINIDVWIKQOLKQLLSAITQDIN-- 238
QY 117 LFKISMLSDVWKQVYALGLOEYLSKQLEKISDLVDVYN-----NVLINSTLTE 167
DB 239 --LTKASTTINSYLVPEIKNLTER-----DGRNLINIPDKLIKQIPLNLYQNTVD 290
QY 168 ITPAYORIKYVNEKEALTSATETMLKTKODSHTDILDELTELAKSVTKNDVGE 227
DB 291 -----QSDVFLKVNIEALINHQPLKQNTWNPINQVND-LSALSNLLEIFETNETNNE 344
QY 228 FYLNTFHDVWIGN-----NLFERSALKTASSELIAKENLKTSSSEVGNVNFILV 276
DB 345 W--NQLITILINHADIDKIEIIRNITSNIIINNAQ--KQDIK--KQIDKIY--LLI 394
QY 277 LTLAQAKAFLLTTCRKLGLADIDYTPIMNEHLN-----EKEFRVNIPLTISNTPS 330
DB 395 KKVLDQY--TLNKSHTSVVKI-----NETIKTLIDSLFANQEIKTLSNTLSNMF 445
QY 331 NPVYKAGSDKDAKIIMEAKPGVALVGEISKDSI-AVLKY----- 372
DB 446 SGNLAKLIVNDEDOQNSL-IRP--VAFIISNDLKIKTLITNTSFIHASELANTPSF 501
QY 373 -----QAKLKNYQ-----IDKSLSEIYVGDIDKLCPDQS-EGMYTNKIA 414
DB 502 BELIVKLISFPQTNLSMLNFIQKILQNDKIDELLAAVIFQKISPOKQVQIQIINK-- 559
QY 415 FPNEVITKIAFTKGLN-----SLRYEVITANFYDSGIDIDANKKIESSEAEFSMLNA 468
DB 560 --DKVVT--FIKKGDNLTFRFDLYNKLNLNLPSSITNOQNTLK-----LLSE 602
QY 469 NNDGVYMPIGTISETFLTPINGFLV-----VDENSLRVTLCKSYLRETLATDSL 521
DB 603 QODSVINIKIIFD-FSPPKQIISLIDVLKNETITSNDYIEVI-KSLDE----- 650
QY 522 KETKLIYPNGFISNIYENGUL-----EGENLEPWKANKKAYVDHTGVNGTKVLY 573
DB 651 -----IDFNHFPQAVGNSMLSNVPLANKHENDSKIDINKYIYV-----KTLF 695
QY 574 VHEDEFSQFIDGKLKTEYVIOYIK--GKAIIYLKDEKNGDYIYEETNNLEDPQAV 631
DB 696 AHENDSTSK--EKLKTIIDELTKKIVENNKKGLLYLNGAIGERT--SNLIINTFPGL 749
QY 632 TKRFTGTDSRVHLIFTSONGEE-----AFGNFTI-----SEIRPSEELSPBLIK 679
DB 750 TN--LKQNYKTLVQKVFNTQMLFBOVONLITYAINSLIDHKNYONCKTFGBELLTTYNK 807
QY 680 SDAWVSGQ-----GTWISGNSL--NINSNVGTFRQULSLESYSTYGMNPNVNGFGKVT 731
DB 808 NQTOQIDKLKAKINKIISGSSSLDEISTSPANTIKYFKLENLTVEDIN-KLSFNFV 866
QY 732 IRNSREVVPEKSYLOPSSKYSI--KFTTTTNNTGILV 767
DB 867 IKNI-----FMLEVNDGLVYKLTITLSNAIKI 894

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## RESULT 5

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T28679
fibrinogen-binding protein homolog - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28679
R:Josefsson, E.; McCrea, K.; Ni Eidhin, D.; O'Connell, D.; Cox, J.; Hook, M.; Foerster, T.
Microbiology 144, 3387-3395, 1998
A:Title: Three new members of the serine-aspartate repeat protein multigene family of S
A:Reference number: Z20510; MUID:99098700; PMID:9884231
A:Accession: T28679
A:Status: preliminary; translated from GB/EMBL/DBJ

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A;Molecule type: DNA  
 A;Residues: 1-1315 <OOS>  
 A;Cross-references: UNIPROT:O86488; UNIPARC:UPI0000052285; EMBL:AJ005646; NID:e1318791;  
 C;Genetics:  
 A;Gene: stdD

Query Match 5.1%; Score 203.5; DB 2; Length 1315;  
 Best Local Similarity 21.3%; Pred. No. 0.11;  
 Matches 178; Conservative 118; Mismatches 305; Indels 235; Gaps 45;

QY 40 NTGSDLTLDLILKQOILNEISGLDGVNSLNDLLAQNLDELSEILKI--ANONK 97  
 DB 139 STIMEDLNTKQITISQEQALQP-----DLOENKSVVAVNOPTNEEK 177  
 QY 98 VLN-----DVNTKLDAL--NMLNT--YLPRKITSMLSDVMKQNALG 135  
 DB 178 KVDKTESSTILNYSDAIKSNDELVLVNNNSNNENNADILPSTA-----PRIN 229  
 QY 136 LQIEYLSKQLEISDKLDVINNVLI--NSTLT-----EITPAYQRIKYNEKEEAL 185  
 DB 230 TRKRIAVNPSSSTEAK--NVNDLITSNTLTVADADKNNKIYVA-----QDIYLSL 277  
 QY 186 TSAENLTKTKQDSHT-----DILDEL--ELTELAKSVTKNDV 223  
 DB 278 KSQITVDKVSQDYFIKTSQVYQYGLNPEDIKIDKPNNGSTIATAKHDYANL 337  
 QY 224 DGEFF--YLNTFHDVMIGNLFGRSALKTASELAKENLKTSGSEGVNFFLIVLALQ 281  
 DB 338 IYTFYDVRNFGVQGINV--SIYMDPTIVSNDVFNITIGT----- 383  
 QY 282 AKAFLLITTCRKLGLADIDYTPIMEHLNKEKEEFVNILPLSNTFS--NPEYK-- 336  
 DB 384 ---TYKTT---ANIQY--DYVNEKNSIGSAFETVSHVGNENKPEGYQTI 428  
 QY 337 ---ARSDDAKTIMEA--KPGVALVGFELISKDSIALVLYQA---KLKNYQIDDSL 387  
 DB 429 YVNSNSLNTNAKLVAVHSSYPNNIGQINKD--VTQIKIYQVKGATLNGVDNNKEL 487  
 QY 388 SEIYVGDIDKLLCPDQEQMYTNKIAFPN--EYVI--TKIAFTKGLSLREYVAF 441  
 DB 488 TDVTNQLQKITVGDNNNAV-----IDFGNADSAVVMWNTKPPQYTNSEPTLVQMTL- 541  
 QY 442 YDSSTGDIIDLKKKIESSEAFPSMLNANDGVMPICGISFTL--TPINGFGLVDENS 499  
 DB 542 --SSTGN--KSVSTGNA--LGFTNNGSGAGQEVYKIGVYVEDTNKKGVDELGKGV 593  
 QY 500 RLVTLLCKSYLRETLATDLSNKEFKLIVP--PNCFISNIYVNGNL--EGENLEPWKANK 556  
 DB 594 GNVTVIVFDNNNTNKGEAVTKEDGSYLIPNLPG--DYRVEFSNLKPGYEVTPSKQGN- 650  
 QY 557 NAVVDHTGVNGTKVLVYHEDGFSQFIQDKLKLTETEVLYQYIVKGAALYILKDEKAGDY 616  
 DB 651 NBEILDSNG--LSSVILVNGKDNLSADLG-----IYKPKYNGDY 687  
 QY 617 IYBETNN--ELBDFOAVTKRFTIGTDSR--VHLIFTSQNGEAF--GNFIISEIR 667  
 DB 688 VMEBTNKGQIQDDDEKGISGVTVTLKDENGVLTAKVTTDADGKXKFFDLNNGYKIVFTT 747  
 QY 668 PSEELSPELIKSDAWGSGGTWISGNSLINSNVNTRFRONLSLES--YSTSMF-- 722  
 DB 748 P--EGYPTTVTSQSDIEK--DSNGLTTGVYINA--DNMTLDGSPFKTPKRYNIGNY 798  
 QY 723 ---NVNGFGK-----VTIRNSREVVERSVYLOFSSSKYISEKFTTTTNT 763  
 DB 799 VMEBTNKGQDSSTEGKISGVTVTLKNEENGVLQTTTDDGKX--QFTGLNGGT 851

RESULT 6  
 T28677  
 rhoptry protein - Plasmodium yoelii  
 C;Species: Plasmodium yoelii  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T28677; C45521

R;Keen, J.; Sinha, K.; Brown, K.; Holder, A.  
 Mol. Biochem. Parasitol. 65, 171-177, 1994  
 A;Title: A gene coding for a high molecular mass rhoptry protein of Plasmodium yoelii.  
 A;Reference number: 220508; MWID:95021522; PMID:7935623  
 A;Accession: T28677  
 A;Status: preliminary; translated from GB/EMBL/DBD  
 A;Molecule type: DNA  
 A;Residues: 1-2269 <KE2>  
 A;Cross-references: UNIPROT:Q26223; UNIPARC:UPI0000080871; EMBL:L27838; NID:g457145; PI  
 A;Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple c  
 Mol. Biochem. Parasitol. 42, 241-246, 1990  
 A;Reference number: A45521; MWID:9101650; PMID:2270106  
 A;Accession: C45521  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 2131-2269 <KE2>  
 A;Cross-references: UNIPARC:UPI000017B646; GB:M34283

Query Match 5.0%; Score 201; DB 2; Length 2269;  
 Best Local Similarity 21.6%; Pred. No. 0.29;  
 Matches 179; Conservative 138; Mismatches 285; Indels 226; Gaps 47;

QY 34 NMIFKTNVGGDLTLDLILKQOILNEISGL-----DGVNSLNDLLAQNLDELSE 87  
 DB 21 SMILKNSG-----ILRKYTISNQIKNDLVSTYPEGREGFTSSL-----ELAKS 65  
 QY 88 ILKIANQONKVLNDVNTKDAINMLNLTVPKITSMLSDVMKQNALGLQIEYLSKQLE 147  
 DB 66 WEKTKLETTTELTKSMEYTRLEKEIRELFK--YLDEAEKYLEGLKLE--LKKIKID 121  
 QY 148 ISDKLDVINNVLI-----NSTLLET--PAYQRIKYNEKEEALTSATETNLTKQD 198  
 DB 122 IIAKIEVKNVTVELKKEIKGNNAVYIDELANQSYKATGYENK-----NTVNTISYFD 176  
 QY 199 SSHTDILDELTELTELAKSTKNDVDFEYVNTFHDVMIGNLFGRSALKTASELIAKE 258  
 DB 177 QIYEGDID--TFYNEISLIVKEDEPIDIE-----DKTKLENL--RSKIDNVYDKIQKM 225  
 QY 259 NLKTSQSEGVN--YNFLIVLTAQAKAFLITTCRKLGLADIDYTPIMEHLNKEKEEF 317  
 DB 226 EITVQSHLNNIETNNKLPNTLILEIKYI-----YBISKE--LNMKLEDF 269  
 QY 318 RVNILPILNTFSNPVEKARSGDKDAKI--IMEAKGVALVGFELISKDSIAVLKVVQAKL 376  
 DB 270 K--NKEKELSNKIS--DYDKRQQLSEYKSMLEIRHYN-----SQTVNDNTKEBA-- 318  
 QY 377 KENYQIDKDSLEIVG--DIDKLLCPDQEQMYTNKIAFPNVEYITKIAFTKGLNSLR 434  
 DB 319 KQNYVDSNEMETIIPNEDEISKIISEVKTMKDEILSKV--NTY-----IDFNKK----- 366  
 QY 435 YEVYANPYDSSTGI-----DLNKKKIESSEAF-----SMLNANDGV--YMPIGTIS 481  
 DB 367 YKETVNSEHSQFTELVDKIAVSDKELKCEQSPDNNSLNETKNSIKETQINNTLK 426  
 QY 482 ETELTPIINGGLVVDENSRLVLTCKSYLRETLATDLSNKEFKLIVPNGFISNIYENG 541  
 DB 427 K-----VDEYIKV-----CKS--TKFSKQITLMDMLNQNIKTYMETN 467  
 QY 542 NLEGNELEPW-----KANNKAAYVDHTG-----GVNGTKVL 572  
 DB 468 SIDKSYIEKEQOILTGKQTLKENKTFEFSILNNEANN--NELIKYFSDLKANLGINNEBML 526  
 QY 573 Y--VHEDGFSQFIQDKLKLTETEVLYQYIVKGAALYILKDEKAGDYIYETNNEL-- 625  
 DB 527 YNQFTEKEKTFNDIKENKIHINEE--ISKIEIKIHASY-----NISETREIGINI 577  
 QY 626 ---EDFOAVTKRFTIGTDSR--VHLIFTSQNGEAFGNFIISIRPSELLSPEL 677  
 DB 578 ESLNTKVFKEKV--KENVTNLIKIKELKHVDF--SDFGKE--GN-----IKYTOKI--KK 624  
 QY 678 IKSDAWVGSGGTWISGNSLINSNVNTRFRONLSLESY-----YSTSMF 722



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Db      625  INDDIMASQ-----QIDQHINGDDIDKSKSEYSEKKEQINLLEKYSNTEISND 675
QY      723  NVNNGGK-----VTIRNSREVVERFSYLDQFSKYSSEKFTTTNTTGL 765
Db      676  NVEGIRKKQOQIIVTKIDKKNIYEE-----INKLLEISIKIEKIDTSL 718

RESULT 7
T18501
hypothetical protein C0760C - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18501
R:Lawson, D.; Bowman, S.; Bartell, B.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z18935
A:Accession: T18501
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3394 <LAW>
A:Cross-references: UNIPROT:O77384; UNIPARC:UPI0000080686; EMBL:Z98551; NID:e1331903; P
A:Map position: 3
A:Note: C0760C

Query Match      5.0%; Score 199; DB 2; Length 3394;
Best Local Similarity 20.6%; Pred. No. 0.61;
Matches 174; Conservative 122; Mismatches 322; Indels 226; Gaps 38;

QY      48  DEIL-----KNOQLNIEISGKLDGVGSLINDLAAQSLDTELSKILKIANQKRYLNDVN 103
Db      1201 DKILRLTKGYQQLLEENYEKIKNNKEKEYLHA---CCKLENNLERNNKEKILLDQGIN 1257
QY      104  TKLDALNMLNTYIPKITSMLSDVKQNYALGLQIEYLSKQKEISDKL--DVINYVNL 160
Db      1258 EKEKKKININEKYI-ILEKEYEEYQNKNI FINAQIELEKEKQLOEIIQDKMINVK-- 1314
QY      161  INSTLTETTPAYQK-----YVNEKPEALTSARETNLTKQDSSHTDIL 205
Db      1315 LNEKKQDILIKYEKQYLTHTLQBNKDSHYLKKQENL----LNLNELKQYDHDHISL 1369
QY      206  DELTELTELAKSVTKNDVGFEPYALTFHDVMIQNLFGRSALTASELAKENILKTSGS 265
Db      1370 NKINTLWLEKKNKK-----NTPH-----MNNL-----RYENNLLKMK 1405
QY      266  EGVGVNYPFLVLTALQAKFLTTCCKLGLADIDYT----PINNEHLNKEKEE-- 317
Db      1406 ELQNKYMIKKELNERIKQINVFNNVSTSLRDNRSRGSIHQINNMYNNTHLGFMA 1465
QY      318  RVNIIPLTISNT-PSNPNYERKAGSDQAKIMEAKGYALVGEISKDSIAVLKYYQA- 374
Db      1466 SKIN-NNISMLYSNNIIMSHRSIIIKNKEDAGNSTQAAAMNKSDTDNI-INNIHTD 1522
QY      375  KLAKNYOIDKDSLEIYVGDIDKLCPDQSEQMYT-----NKIAFPNEYITTKIAFPKL 430
Db      1523 NINNMNINNNNTLNSI-----NSNHLIYPPFPNNNVNSPFGVGMCDVTLASGV 1570
QY      431  NS-----LRYEVTAN-----FY 442
Db      1571 NKQDPLLNLEENENSFLVEYELRIKSLQELCDKESIIKIKGEKNILITCIETWKCFC 1630
QY      443  DSGTGDJ-----DLNKKKIESEAEFSMLANNQGVWPIGTISFTPLTPINGGLVYDEN 498
Db      1631 KNSKEEELSLRAKEIGKEQLEKHK-EFLINKSN-----EDKLKTYIN-SLGLDEK 1676
QY      499  SR--LVTLTKCSYLRETL--LATDLSNK--ETKLIVPNGFI--SNIVENGULEGENTL 549
Db      1677 DKYDIVVDIKNNRNEIDKLNDINSEKYEIKLLKHENNNLINENMILLNKKKEIENNNIK 1736
QY      550  PW-----KANNKNAVVD-----HTGCVNGTKVLY-----VHEDGFSGFIDCKL 588
Db      1737 QKEEDYKLIKQDQTNIQNEYNDELLEKYNEVYVAKNNMLYNDMNVLLKEHEBEIIFLKENI 1796

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[illegible]

QY 142 SKQKLEISDKLDVINNVNLINSLTEITPAYQRIKYVNEKEEALTSATENLTKTKODSSH 201  
Db YENKQ--NNSVDYDIIINFLSNYPFKYDICKLNCKENNNNNKMAI--GATDIN----- 240  
QY 202 TDIDDELTE--LTSLASVTKNDVDGFEFYANTFHDWIGNLFGRBALTKASLLAKEN 259  
Db 241 -----TENILNKLKLS-----YY--YQELIQTN-----LAAASDILRIAI 274  
QY 260 LKTSGEVGNVYNFLIVLTALQAKAFLLTTCRKLGLADIIDYTPIMNHELNKEKEFRV 319  
Db 275 LK-----KYGQY-----CQDPLPGVN----- 292  
QY 320 NILEPLNTSNGNPEYKARGSD--DAKIMEAKPGYALVGFISKDSIALVKYQAKL 376  
Db 293 ---LSLENDISKPN-----GMDSNYMEALP-----EALA-----NEKKL 324  
QY 377 KHN-----QIKDLSSEIYVGDIDKLCP-----DOSEQWY-----YTNNKAF 415  
Db 325 MANNPYRYMEQVSEIERILISFVRNHDINDLILPLGDIKISQLEILSLKAAATGKKT 384  
QY 416 PNEVIT--KIAFTKLNLS--RYEVLANF-----YDSSTGIDILNKKIESSE 460  
Db 385 SNAIISNNDSLNLNLSQLENNYEILNLSIQEKFKICEYDYSYNSV--SELVLETP 442  
QY 461 AEFSLMANNDGYMP--IGTISETFPLPING-----FGLVV 495  
Db 443 KNLSM--DGSSFYQOIIIGYLSGFKPEVNSTVFSGPNYSSATCDTYHFKNTPML 499  
QY 496 DENSLVLTNCKSLRET-----LLATDLSNKE--TKLIVPNGPISNVEKNLEGE 546  
Db 500 SONEIPEASNNLTFSSKTHDEFFKSSWLSRNLIAKEQKLTGYIGTLNTE---DGL 554  
QY 547 NLEPMKANNAAYVDHTGCVNGTKVLYVHEDEFSQFIGDKLKLCT-----EYV 595  
Db 555 NFNMKQVLTSELLKVLBEVNSTKIYENYDLMILQIQGDDISYESAVNVPKPKNSIL 614  
QY 596 IQYIVKGAALYVKDEKNGDYIYETNNELEDFOAVTKRPITGTDSSRVHLIFTSQ--G 653  
Db 615 IOGVDDPANYFYF--ENGIVQSDININNIISRFNDIKIKILT-----LIGHGEVFN 663  
QY 654 BEARGNFI-----ISEIRPS--EELISPELTKSDAMVSGQWISGNSLNTN----- 699  
Db 664 PKLFGKTVNDLNTIITKPKLQHLERB-----GYLNKKYKLNKILQCYMFP 712  
QY 700 -SNVNGTF-----KQNLSESYSTYSNMFNNGFKVYIIRNSREVEERSYLQFSSK 750  
Db 713 KVDINSTFVGKLFKISRDLQPKGFSKNGQLEISAN--KYAIRINR--GKREVLDFYFK 767  
QY 751 YISEKFTTTNNNGLYVELSRASRGVINFCD 782  
Db 768 WVS-----NTDLIAE--QISNKYVYVWNE 789

RESULT 9  
C97033  
uncharacterized protein, probably surface-located [imported] - Clostridium acetobutylicum  
C/Species: Clostridium acetobutylicum  
C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: C97033  
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Benmett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld  
A/Reference number: A96900; MUID:21359325; PMID:21359325  
A/Accession: C97033  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1227 <R>  
A/Cross-references: UNIPROT:Q97K41; UNIPARC:UPI0000CA0A1; GB:AE001437; PIDN:AAK79054.1;  
A/Experimental source: Clostridium acetobutylicum ATCC624  
C/Genetics:  
A/Gene: CAC1080

Query Match 4.9%; Score 194; DB 2; Length 1227;  
Best Local Similarity 19.6%; Pred. No. 0.26;  
Matches 173; Conservative 146; Mismatches 320; Indels 242; Gaps 45;  
QY 9 VKALPSFDVFNIGYATGATGKIDIMNIFKTNNGD--LTLDELKQ--QLNEISGKL 64  
Db 416 VKEVKTLIDFYNNHAAAGQITLQDKVNDPNAQVQDDVALTSMLKTRDCKTLKALODKI 475  
QY 65 DGVNGSLNDLAAQ--GNLD-----TE-----LSKEIILKANEQNK-----VLNDV 102  
Db 476 DSIINSLKINSGINSGINDYDYSKQTEAVDASKLEAVNDLKKIKADGRDLTIOERISV 535  
QY 103 NTKLDALINMLANTYLPKITSMLSDVMKONTALG-----LQIEVLSKQLEISDKLDVIN 156  
Db 536 KTIIDYINSTN--VSKDGSVSDYI-----TIGIDGTEINIFVNRIRKESGITTIEN 589  
QY 157 VNNLINSTLREIPAYQRI-----KYNEKEEALTSATEN-----LTKQDSSHTDI 204  
Db 590 IKVVI--EPVQLEEVYRIYGVGVVDYKTLGINNVNDNNIYINAEINKKDKDVKIQDI 648  
QY 205 ---LDELTELTELAKSVTKADV--DGFEF-----YLNTPHDWIGNNLFGRSA 247  
Db 649 QTRVDNTINNIDYINKIAGADVALSDYFNIGITDYODIIDYVNA--DLKIQN----- 699  
QY 248 LKTASSELLAKENLKTSGSEVGNVYNFLIVLTALQAKAFLLTTCRKLGLADIIDYTPIMN 307  
Db 700 YKQVDIIEHVEAKIS--YEALMRINIGEA-----VTDDPKALGLTDIN----- 742  
QY 308 EHLNKEEBERVNIPLTSLTSPNPNYKARGSDKAKIIMEAKPGYALVGFISKDSIA 367  
Db 743 -----DGLLVATDLOKNKYTKAD-----EVIARVQA 770  
QY 368 VLKYYQAKLKANYQIDKDSSEIYVGDIDKLCPDQSEQ--MYTNKIAFPNEVYTKIAF 426  
Db 771 QIEIYRLMGIN-----LGKATADYNTLGIIDVNDLSILTYVNDLQGRVY----- 817  
QY 427 TKKLSIRLYEVYANF-----YDSSTGIDILNKKIKIES--EAEFSLMANNDGYM 475  
Db 818 --NVDEVKAEIERKNIQYVNLMLKIDSGSATID--DYRTIGITVYIDYINISYVIRIKQMI 874  
QY 476 PIGISTEFTLPINGFGLVYDENSRLVLTCKSYLAETTLATDLSNETGLIYPPNPFIS 535  
Db 875 PVSVDARFPIITILN--NMIVSVSGTIT-----DSATGTPLOGEVIERFRGEN--- 921  
QY 536 NIVENGNLEGENLEPMKANKNAAYVDHTGCVN-----GTKVLYVHEDEFSQ--FIGDKL 588  
Db 922 NIA--GNYFSKNSPYEAT-----VDAQKYSIQLEPGSYTVAIKXDDGYTQNFVITSNG 974  
QY 589 KAKT-----EYVIQYVK-----GKAAIYL--KDEKNGDYIYEETNNELED 627  
Db 975 KAKTVLQNIQVLNMLQYTVSGVVDQAQTNPLQGVAIRFRIGQNKSGDY--YSVNGEYVV 1033  
QY 628 FOAVTKRFIGTQSS-----RYHLIFTSQNGEAFPGNFIISIRSEBELSP 675  
Db 1034 YTDAQKRYTSLSDGYTAFAKKGYINVSVAISSEATNNIQTIVISQTL--SENOYRV 1092  
QY 676 ELIKSDAMVSGQGTWISGNSLINSNNGVGFRRONLSLESY-----STYSNMFVN 725  
Db 1093 VL-----TW--GANLDDLDSHFSGSGGQGINVYQAPSAQVGDYVSLDIDAK 1140  
QY 726 -GFGKVTIRNSREVEERSYLQFSSKYISKFTTTNNNTGL 765  
Db 1141 FGVPETV--TVVDKSGSYTVSPDFSGSSASAKLSL 1178

RESULT 10  
G82887  
hypothetical protein U7474 [imported] - Ureaplasma urealyticum  
C/Species: Ureaplasma urealyticum  
C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C/Accession: G82887  
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Casseall, G.H.  
submitted to Genbank, February 2000

A>Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mit  
A:Reference number: A82870  
A:Accession: G82887  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1313 <GUA>  
A:Cross-references: UNIPARC:UPI00000C1C82; GB:AE002143; GB:AF222894; NID:g6899457; PIDN:  
A:Experimental source: serovar 3; biovar 1  
A:Genetics:  
A:Gene: UU474  
A:Genetic code: SGC3

Query Match 4.8%; Score 193.5; DB 2; Length 1313;  
Best Local Similarity 21.0%; Pred. No. 0.3;  
Matches 185; Conservative 146; Mismatches 291; Indels 261; Gaps 52;

29 IKDMMMF---KTNNGDGLTD-ELIKNOQLNEIS-----GKLDGVNSL 71  
180 LKDLHNHYKKTAKSNMGEVSPDSQKNNLYEVIALQTDQTKIVNVEIEYNNKII 239  
72 NDLLAQNLID-----TELSKEILKIANEO-NKYLVNDVNTK---LDAIN--- 110  
240 NNL-----NIDELNTPYQYKNGHNLAKIPRYANEQYGVFEDQNNQKHLIPAVNKD 295  
111 --LMLNTYL---PKITSLSDVM---KONYALGLQIEYLSKQLEISDK-LDVINAVVL 160  
296 GTIMEDFQVLTKNPKKYHLQKVYLAQNQOILHNPLVSNQKODIFLKKYKVISAL 355  
161 IN---STLTETTPAYORK--YNEKFPALTSAETTNLKTQDSHTDILDELTELTA 215  
356 ENDADKTKREINLKLKSNKMWNVKQIKVIYSSSGS-----DVQTPPLVLE 402  
216 KSVTK-----NDVGFBEFLYTFHDV-MIGNNLFGRSALK-----TSELAKEN--LKT 262  
403 KNGQNYVYKLNKLNKLNRLY--TLKAVEILINN--GKTNLPDITNLSFWERTSAVAT 458  
263 SGSEGVNVNPLVLTALQAKAFLTLTCRKLGLADIDYTPIMNE-----HLNKEKEF 317  
459 SISISN-----RLGATLTNAQVKITLKQDVNLVLANQKAIYNGNQQSEA 505  
318 RV-----NILPLTSLN-TESNPNYKARSGDKAKIMEAKPGYALVGEFISK-DSTAV 368  
506 TVIVNNGVKYLIATLTKLTMTPTIKS-----LTFEOKPTCALEINIGLDTNNIY 557  
369 LKYYQAK-----LKNAYOID-----KDSIEIYVGIDIKLCPQOSEMYTNTKIAF--- 415  
558 QNTHAALPLVYINNPFINGPLASHESLSKINSADAKV-----NAINITLD 605  
416 --PNEYVITKIAFTKQNSLRYEYANFYDST---GDIDLNKKKIESSEAFSMLNAN 470  
606 FNTNHHYKQLFFFLKTVPIDDQGNENIYDSEAIYSDV-LSANNITANKIQFSLGHLQ 664  
471 DGVMPIGTI---SETFLPIPGFGLVVDENSRLVTLTKSYLRETLATDLSNKEKTL 526  
665 NRRKX-KKTIYYLTSKT--TPLDHNVVMIK-----PNVXSEI 699  
527 IVPNGFIISNVEGNLEBMLBPMKANNKAAVVDHGVNGTKVLY--HEDEBSQFI 584  
700 IYVAND--STIVKYGNNMDSI-----TNGSKAFKINCNDSD---IL 737  
585 GDKLKLKTEY-----VIOYIVKGAALYLKDEKNDYIYEFTNNELEDFQAVTKRFT 637  
738 SEDLSATLVYESNDPHLOSTYTKL-----KVNNDWVIDPMLNLKPQTYTHLKSIT 790  
638 GTDSSRVHLFTSQNGEBARGFNFISEIRPSEELLPELIKSDAWGSGQ-TWIS-GNS 695  
791 IAKENKAYTNLKIOS-----LPQVDIKTQL--PNLIHDLKATSAVLKWDSTNNG 838  
696 LINSNVNGFR-----QNLISLSTYSNMFVNVNFGK--VYIIRSREY-----V 739  
839 KNNHQIQATFSHVSANAYDNLVKLYEYNRGDIKAVESDILTLLKQDQVYQINLPISV 898  
740 FERSYLOFSSKYISEKFTTTNTNGLVVELSRASSRGVINFGD 782

Db 899 PNRKY-TEKVTYLDER-----NNLNMYDNLKK-----INLTD 930

RESULT 11  
G82934  
hypochemical protein UU094 [imported] - Ureaplasma urealyticum  
C:Species: Ureaplasma urealyticum  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
A:Accession: G82934  
R:Glass, J.I.; Letkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Casselli, G.H.  
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a m  
A:Reference number: A82870  
A:Accession: G82934  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1054 <GUA>  
A:Cross-references: UNIPARC:UPI00000C1B96; GB:AE002109; GB:AF222894; NID:g689945; PIDN:  
A:Experimental source: serovar 3; biovar 1  
A:Genetics:  
A:Gene: UU094  
A:Genetic code: SGC3

Query Match 4.7%; Score 189.5; DB 2; Length 1054;  
Best Local Similarity 21.3%; Pred. No. 0.34; Mismatches 292; Indels 225; Gaps 40;

18 YF-----NGYGFATGIDKIMMIFKTYGDL-FLDEILKN-----QQLNEI----- 60  
332 YFGANSNEKPSFGHSTYTLNNEIQASVEODIFSLDKIKNELKKNBQILKQIEVAF 391  
61 SG---KLDGVNSLNDLLAQNLDELTELSKELK-IANBQNKVLNDVNTKDAINMLN-T 115  
392 SGYVAIDISGISIN-----ILKGVANDMLKELFLQSSQDFRMLTYAIT 436  
116 YLPKITSMLSDVMKONYALGLQIEYLSKQLEI---SDKLDVINAVNLINSTLEIRPAY 172  
437 QQNNLTULIT-LITSNQSGLVAVIDGFKPILKEIYNNPSIDQ-SVKQTIISKIDSMDFKN 494  
173 QRIKYNEKEALTSATETNLKTQDSHTDILDELTELTAHSVTKND-----VDG- 225  
495 NLMEIQIRTLDSISLTKIT-----YKPIIKLELISLEARSKOPKNGVPIDGL 549  
226 ---PEFLANTPHVMIGNNLFGSALKTASBELAKENLKTSGSEGVNVNPLVLTALQA 282  
550 DELPSFLN-----LK-QNDLPSISINFKI-GQQNYLYLD----- 582  
283 KAFVLTTCRKLGLADIDYTPIMNEHLNKEKEF-----RVNLTPLIS-NTFSPNY 334  
583 -----ITVEKKIAN---NLIPHENQYDPKQOQIISTNYFLTKIIDLISLNKNDQLDY 633  
335 EKARGSDKAKIMEAKPGYALVGEFISKQIA---VLKYYQAKLKHNYQIDKDSLEI 390  
634 HK-----GVEIMFSLKKRQIAPREIYKIIDIBELLQNTNMKNKENIKKL 677  
391 VYGDIDKLLCPDQSEQMYTNTKIAFPNEYVITKIAF-----KQCN-SLRYE 436  
678 ---LDAILYKITSNDPSINDLSKYPKGISKREITSKELEYDQNNLLIKLNLIKRYRK 733  
437 VTANFYDSSGDIIDLNKKIES-----SEAFSMLNANDGVMPICITSETF 484  
734 VLNAAEFDIKPLPDLPOKPLSFTDLGLMEQIKKEPPYKIVLAKNDYVHTTISISOPB 793  
485 LTFPIPGFGLVVDENSRLVTLTKSYLRETLATDLSNKE-----TKLIVPNG 532  
794 LT-----TLIFDRSDHDKKXKGYVYPTHTYQTNHNS 827  
533 FISNIYENGLBEBNLEBPMKANNKAAVVDH-TGCVNGTKVLYVHEDEBSQFIQDKLKL 591  
828 -MKAIITENISLRNDRLLP-----NKKYVAQLMMLFVKKQVFINPLAIYETFFGDK-KIP 879  
592 TEVVIQYIVKGAALYLKDEKNDYI---YEFTNNELEDFQAVTKRFTIGTDSRVHLI 647

Db 880 NDKKVKLLIDONLNKYLKNDKSDNTYCEGPFKHFSSNNLEN--KVGQTIENLILAKIKTI 937  
QY 648 FTSONGEE-----AFGNGFIISSEIRSEELISPELI-----KSNAMWGSQGTWISGN 694  
Db 938 KT--DGGELYODALGKKIATISAYDQJNLTLQELIDYKLLFGGKRVL---KKDVLISAV 992  
QY 695 SLNINSVNGTFRONLSLESYSTYSNNPNVNGFGKVTI 732  
Db 993 AFNPGINTNDSQTNV---LNNDEIKYNNILKKVVI 1027

## RESULT 12

T30822  
Impli protein - Mycoplasma hominis  
C/Species: Mycoplasma hominis  
C/Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T30822  
R/Jensen, L.T.; Ladefoged, S.; Birkelund, S.; Christiansen, G.  
Infect. Immun. 63, 3336-3347, 1995  
A/Title: Selection of Mycoplasma hominis PG21 deletion mutants by cultivation in the pre  
A/Reference number: Z18884; MUID:95369882; PMID:7543881  
A/Accession: T30822  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1365 <JEN>  
A/Cross-references: UNIPROT:Q49525; UNIPARC:UPI00000BC623; EMBL:U21962; NID:G790243; PII  
A/Genetic: A;Gene: Impli  
A/genetic code: SGC3

Query Match 4.7%; Score 189.5; DB 2; Length 1365;

Best Local Similarity 18.5%; Pred. No. 0.48;

Matches 171; Conservative 137; Mismatches 317; Indels 299; Gaps 39;

QY 1 MQQNNKLSTVALPSFID-----YFNGIYGPATGIDIMNNIFCTNT 41  
Db 553 IKSNNTASWQSAKSSLDKAVAEITKLETENKDEAKFNEIKQTRNQIOEFIN-TNNKNP 611  
QY 42 GGDULTDEILKNQOLNEIS-----GKLDGVNSINDLLAQNDLTLSKEIILKINEO- 95  
Db 612 NYSELLSQLTSSKDSKDSVTDSSNKSDDIESANTELKQALAKANADKYQALNLASIKEQ- 671  
QY 96 NKVLNDVNTKLDALINIMLNTYLPKITSMLSDVMKONYAL-----GLQI--EYLSQOLKE 147  
Db 672 NNSVSNANTISAKLTQDKDNTIQQAKTELEKEIQKANAISNTTASWQSAKSSLDKAVAE 731  
QY 148 ISDKLDVIN-----VNLINSTLTETTPAY-ORIKYNEKFEALTSAT- 190  
Db 732 ITKKLETFNKDEKAFNEIKQTRNQIOEFINT--NKNPNVSELLSQLTSSKDSKDSVTD 789  
QY 191 TNNKTQDSSHTDIDBELTELAKSV-----TKND-----VDGFEFYINTPH----- 234  
Db 790 SSNKSDDIESANTELKQALNTAKAKSSIDNELRLPKDLOSKEEPFIRNTNFSWISK 849  
QY 235 -----DVMIGNNLFGRSALKTASELIAK-----ENLKTSGSEVGVN----- 270  
Db 850 LETTKNKLABELTKRADIKNNPSSSKQALMDSQGVQKLGNEILKITEEFGVETKSN 909  
QY 271 --YNFLIVTALQAKAF-----LTLTCKKLGLADIDYTPIMNEHLNK 312  
Db 910 IGR--LFLKLAQAEQFNNSDVKLKNAMWEKQTLSSKQKLGQSTKYDYLTQ-STEMST 966  
QY 313 EKEEFVNILPTLSNTPNENYKARGSDAKIKMEAKPGYALVGEISKDSIAVLKGY 372  
Db 967 QESTIKKYIVNIQAHIRNNLNSQTRLEAD--KLIANMKRGYG-----DKVGIESLQWK 1017  
QY 373 QAKLKNNYQIDKDSLSE-----IYVDIDKLCPCDSEQMYTNNK----- 412  
Db 1018 QDLMDSDVLSVDLSKODFNKALRVLVGDVTK---NPPVSSWFINKRNSIENYQNLN 1073  
QY 413 --IAPNEVYITTKIAFTKGLNSLRVEYVIANFYDSSCTDIDLNKKKIESSSAEFSMLANN 470

Db 1074 LILVRENEILLDK---AKDLK--RAEKTIKFDVENINSISLDQAKRLKQ-----EILNAKN 1124  
QY 471 DGVYMPIGTISERFLPPINGFGLVVDENSLVTLTCKSYLRETLATDLSNKETKLIVP 530  
Db 1125 D-----LSNFTL-----NKKNOFTAKDITPK----- 1146  
QY 531 NGFISNIVENGLEGNLEBPWKANRNAVVDHTGVNGTKVLVYHEDGSPQFIDKCLK 590  
Db 1147 ----ISLEN-----KLEINQY----- 1160  
QY 591 KTEYVIQYVKGAAAYLADKNGDYIYEETNNELEDPOAVTKRPTITGIDSSVHLIFTS 630  
Db 1161 ----LPLIKERKAVKISE-----IKKKKELEDI--IRSNFYLM--EKVEI---- 1199  
QY 651 QNGBEAFGNGFIISSEIRSEELISPELISDAVWGSQGTWISGNISNINSVNGTFRONL 710  
Db 1200 -----NKYISETLNKQVLEIRSNINPENKESIKDTL--DNLNKENVS--LLEKVI 1246  
QY 711 SLESYSTYSNN--FVNGFGKV-----TIRNSREVPERSYLOFS-----SKYISE 754  
Db 1247 INNSNQYSINRLSTVPERIKVAQTRRSNNLSLAEIQKPTLLIDKVLKEVKKILDE 1306  
QY 755 KFTTTNNTG-----LYEELSR 771  
Db 1307 NKTLSNDNIAKLNKIKRLVDRSR 1330

## RESULT 13

ORF MSV156 hypothetical protein - Melanoplus sanguinipes entomopoxvirus

C/Species: Melanoplus sanguinipes entomopoxvirus

C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004

C/Accession: T28317

R/Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.

J. Virol. 73, 533-552, 1999

A/Title: The genome of Melanoplus sanguinipes entomopoxvirus.

A/Reference number: Z20484; MUID:99102612; PMID:9847359

A/Accession: T28317

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1127 <AF0-

A/Cross-references: UNIPROT:Q9YVT6; UNIPARC:UPI00000F6900; EMBL:AF063866; NID:G4049647;

A/Genetic: A;Note: MSV156

Query Match 4.7%; Score 189; DB 2; Length 1127;

Best Local Similarity 19.4%; Pred. No. 0.39;

Matches 161; Conservative 150; Mismatches 290; Indels 230; Gaps 38;

QY 31 DINMMIFKTNTGDLTL-DEILKN-----OOLNIEISGKLDGVNSIND----- 73  
Db 168 DIANKLKLVSSPEKQILQIYNNINKKEIFFNQKINQVKEINKKQDELKLDDESKER 227  
QY 74 LLAQNDTELK--EILKIAN-----EQNVLNDVNTYKDALINL---MLNTYL 117  
Db 228 IKQSEELNKTIQKQEBELIKKLDKEINFNIDEKQTLQJNSKINTLNIENIGVANNLYT 287  
QY 118 P---KTSMLSDVMKONYALGLQIEVLSQOLK--ISKLD--VINAVNLINSTLTET 169  
Db 288 ETKNKISNLQNEILNDOSTI-----KSLDEKQKLDLBDKNINNTISLVKSSYTKIT 339  
QY 170 PAYQRIKYVNEKEALTSATETNLKTKQDSSHTDIDDELTELAKSVTKNDVDPEFY 229  
Db 340 NIOQLLE-----SSLTDFNNANNINNELSKIKLKD--NDIQKLNNDITEQNNKLTDF 391  
QY 230 LNTFHDVMIGNLFGSALKTASELJAKENLKTSGSEVGVNVTNFLIVTALQAKAFLTLT 289  
Db 392 NN-----STRIFKEKLDTEYKIKDIDIKNNNLQKLESEYKXIDEQ 431  
QY 290 TCKKLGLADIDYTPIM--NEHLNKEKEFRV-----NILPTLSNTP 329  
Db 432 EYTK--NKINKENYDILIELKNNVLQKLEENKKIDQETEVYKNNKINKENYDILIELKNNL 489

```
QY 330 SNPTEKARGSDKAKIMEARPGYALVGFESISKDSIALVKYQ---AKLKINY-QIDKD 385
D 490 QKLEBENKINDKLTAKLNDIESNTL-----FNKLNISDPFKDSREIAKLNTREYQLRD 545
QY 386 SLSEIVGDDIDKLCPDSEQMYNNKIAFPNEVITTKIAFTKLANSLREVTANFYDSS 445
D 546 LLENI-----NK-----TNE-LMKLS-DNKLSLE-----QLYDS- 573
QY 446 TGDIDLNKKIESSAEFSEMLNANDGVYPIGTISEFTLPINGGLV-VDENSRLVTL 504
D 574 -----KNIIDGIDIKINSLKSKDKI-----DEFNSIEKFDIYNVENFIGNL 619
QY 505 TCKSYLRETLATDLSNKKETLIVPNEGFINIVENGMLGEBNLEPWKANNKAAVYDHTG 564
D 620 -----DSIIKKIINNDQFK-----EYINSKIDSKSNELSTWDDIIFNAQOJASTIN 666
QY 565 GVGNGTKLVYHEDGFSQPIGDKLKLTREYVQYIVKGAAL-YLKDEKNGDYIEETN 622
D 667 NIEN-----ISNKIKDLNEFIISNEDSSKELDEIRKRYQCFDKIKDAMN 711
QY 623 NELEDFOAVTKRFTITGDSRVHLIFTSQNGEAFGNFIISIRPSEBELLISDA 682
D 712 TEVSFETLQKDIDISIKSN-----INELTNAYDITNTKANDDD 751
QY 683 WVGSGTWISGNSLININSVNGTFRONLS-----LESYSTSMNFN-VNGFGKVT 731
D 752 KLNNGSEBFK-NLYNNASDLDLDTIQKNDEKVKQLEKKNKNSIENDIVNNFIEL 810
QY 732 IR-NSREVPERSVYQFSSKYSIEKFTTTTNT---GLYVELSRASSRCVI 778
D 811 IKFNNTS-----TNKSLNELLTNDIDINDIKIFKLYKEIKINSTNLL 851
```

## RESULT 14

```
Imp1 proteain - Mycoplasma hominis
C/Species: Mycoplasma hominis
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T18351
R Jensen, L.T.; ladefoged, S.; Birkelund, S.; Christensen, G.
Infect. Immun. 63, 3336-3347, 1995
A/Title: Selection of Mycoplasma hominis Pcz1 deletion mutants by cultivation in the pre
A/Reference number: Z18884; MUID:9536982; PMID:7543881
A/Accession: T18351
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1051 <JEN>
A/Cross-references: UNIPROT:Q49524; UNIPARC:UPI00000B95B; EMBL:U21961; NID:9790241; PID
A/Genetic code: SGC3
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```
Query Match 4.7%; Score 187.5; DB 2; Length 1051;
Beet Local Similarity 18.6%; Pred. No. 0.41;
Matches 171; Conservative 135; Mismatches 316; Indels 289; Gaps 39;

QY 4 NKKLSVKALPSPID-----YNGIYGRATGKIDIMNMFKNTNGD 44
D 242 NNTASQSAKSLDAKVAETKGETFNKDKAEKNEIKQTRNOIQEFIN-TNNKNPYVS 300
QY 45 LTLDELKNOQLNEIS-----GKLDVNGSLINDLLAQNLDTELSEIKLIANEQ-NKV 98
D 301 ELISQLTSKRDSKNSVTSNKSQDESANTBELKQALAKANDKYQADWLASIKQNLNS 360
QY 99 LNDVTKLDAINMLNTYLPKITSMLSDVKONTAL-----GLQI-EYLSKOLKEISD 150
D 361 VSNNTYLSAKLTDKONTIOAKTELEKEIQKANOAIKSNNTASQSAKSLDAKVAETK 420
QY 151 KLDVYN-----VNVINSTLTLEITPAY-QRIKYVNEFEALTSATETNL 193
D 421 KLEFPNCKEAKNEBKTRNOIQEFINT--NKNPNYSELISQLTGRDSKNSVTSN 478
QY 194 KTKODSSHTDILDELTELTELAKSV-----TKND-----VDGFERYLNTFFH----- 234
```

```
D 479 KSDISANTELKQALNTAKAKKSSIDNELRPLKNDLQSGKIEBFGRIRNTNFSWISSKLET 538
QY 225 -----DWNIGNNLGRSALKTASBLIAF---ENLTKSSGSEGVN-----Y 271
D 539 TKNKLAEELTYRADAIKNNPSSSKQALKDSOQVOQLGNEELTKTIEEFKGETKNSNIGY 598
QY 272 NFLIVLTLQAKAF-----LTLTCRKLGLGADI DYPIIMHELNKKE 315
D 599 R---LFLKAOEQRNNSVVDKILKANWEKQTLISKQKLGNOSTQVYLTQJSTENSTDES 655
QY 316 EFRVNLPLTSTFSPNYEKARGSDKAKIMEARPGYALVGFESISKDSIALVKYQAK 375
D 656 TIKKVTIVIQAHIRNNLNSQYRLND---KLIANKRGYG-----DKVIGESLQKMDL 706
QY 376 LKANTYQIDKDSLSE-----IVGDDIKLCPDQSEQMYNNK-----I 413
D 707 MDSVLSYDSDSLKDFNKLALVVLVDYTK---NPPVSWFINKNRSIENYQNLRLNLT 762
QY 414 AFPNEVITTKIAFTKQNSLREVTANFYDSTGDDIDLNKKIESSAEFSEMLNANDGV 473
D 763 VRENELTDK---AKDLDK-PAEKTIKFVDENINSLDQRAKLRQ---ETLNKND-- 811
QY 474 YMPIGTISEFTLPINGGLVVDENSRVLVTFCKSYLAEETLATDLSNKKETGLIVPNGF 533
D 812 -----LSNFTL-----NHQNGQFADIDTPK----- 832
QY 534 ISNIVENGNLGENLEPWKANNKAAVYDHTGNGTKVLVYHEDGFSQPIGDKLKATE 593
D 833 -ISLEN-----KLANEINQY----- 846
QY 594 YVIOYIVKRAIYLIKDEKNDYIEETNNELEDFOAVTKRFTITGDSRVHLIFTSQNG 653
D 847 --LPLIKEKAVSKISF-----IEKKKKELEDI--IRSNFYLM--EKVEI-- 885
QY 654 EEARFGNFIISIRPSEBELLISPEIKSDAVNGSGTWSGNSLININSVNGTFRONLSLE 713
D 886 -----NKYISELNTKQVLELNSNINFEKMSISDTL---DNLNIKEVVS-LIKEVIINN 935
QY 714 SYSTYSNM---FNVNGFGK-----TIRNSREVPERSVYQFS---SKYISEKFT 757
D 936 SNAQYSIRILISTYBPEFIKVAQTTRSNMLRSIABIQFETPLDIDKILKEVKKLIDENKT 995
QY 758 TTTNNTG-----LYVELSR 771
D 996 LNSDNIAKNEKIRLVLDRSR 1016
```

## RESULT 15

```
B82909
Conserved hypothetical U0292 [imported] - Ureaplasma urealyticum
C/Species: Ureaplasma urealyticum
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C/Accession: B82909
R Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Helner, C.R.; Chen, E.Y.; Caswell, G.H.
Submitted to GenBank, February 2000
A/Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mi
A/Reference number: A82870
A/Accession: B82909
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1830 <GLA>
A/Cross-references: UNIPARC:UPI00000C1C05; GB:AE002127; GB:AF222894; NID:96899268; PIDN
A/Experimental source: serovar 3; biovar 1
A/Genetic code: SGC3
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Query Match 4.7%; Score 187; DB 2; Length 1830;
Beet Local Similarity 20.2%; Pred. No. 0.93;
Matches 173; Conservative 139; Mismatches 276; Indels 270; Gaps 43;

QY 20 NGIYFATGKIDIMNMFKNTNGDILTDELK---NQQLNEISGLDG-VNGSLNDLL 75
```

Db 561 NNIGTONISKILYDVERKNIINDONUYELIKGMFHSQLPFNENKSQIKSLIKALISDLV 620  
Qy 76 AQGNL-----DTELSKEILKIANE--QNKVL-NDVNTKLDAINMLNTYL 117  
Db 621 SSHKLBIIIGFEATDNLKONNEFLKNLIIQNKLTQTSJLDNIINWFDALFPDNDNEYL 680  
Qy 118 PK--ITSMLSDVMEKONYA-IGLQIEYLSKQKEISDKLDVINAVLI-----161  
Db 681 LQGPLSNVLAKIVTKNALLTRIDNLFNDLFXQQTILDA-TYNILIRVQGNIPDFIKT 739  
Qy 162 ---NSTTEITPAYQRIKYNE-KFEALTSATETNLTKQ---DSHTDIIDELTE---210  
Db 740 PQAHLIKKILSKGTNKLINTLKLNTIDLLTDS--KYVAGIFDSSETSIIINLIQKSIDF 797  
Qy 211 ----LTELAKSVTKNDVDGFEFLNTPHDVMIGNNLFGRSALKTASELIAKENLKT--S 263  
Db 798 TSXSFISDVDDLTSNDV-----LNEM-----KEFIKTIYN 829  
Qy 264 GSEVGNYVNFIV-----LTALQAKAFLTLTCKRLG-LADIDYTPIMNEHINKKEE 316  
Db 830 SSTIKNIFNGIIVLVSNNTPLKTSHPDEFVLLKNLIAVLEKDWI-----TNQKX 882  
Qy 317 FRVNILFTLSNTFSNPNYEKARSGDKAKIIMEAKPGYALVGFEISKOSIAVLKVQAKL 376  
Db 883 LKSLIRMSVDLKNPQTONFVTSIED-----FANKLGDLVISANNSLL 927  
Qy 377 KHNVOIKDLSLSEIVGDIDKLCPDQSEQVYTNKIAFPREVITIKIAFTKDLNLSLRYE 436  
Db 928 KSN-----MSDIWKL-----KEVVDLHSSSESYDLIFS 957  
Qy 437 VTANF-----YDSSTGIDIL-----NKKIESSEAEFSMLANNQVYMPIGTISE 482  
Db 958 IINDFIHPQNYDNLNINIDLPLIKSTNKELODKVDILFKL-INNENIPNLVGTLT- 1015  
Qy 483 TFLTPINGF--GLVVDENSRLVLTCKSYLRETLATDLSNKETKLIVPNGFISNIVEN 540  
Db 1016 TNLIVKNPFVVELTVDOKOKI-----NNFTNILLPT 1046  
Qy 541 GNLEGENLEPMKANNKNAVYDHGCVNGTV-----LYVHEDGFSGQFIGDKL-KLKTBY 594  
Db 1047 ----TPNLTLYKEIRKQAFELTNINKILVDPKNTLLILNDG-INKLISNILPOLST-- 1099  
Qy 595 VIQYIVGKAAYLKDEKNGDYIEETNNELEDFQAVTKRPTIGTDSRVHLIFTSQNGE 654  
Db 1100 LIEIDNDK---IKD-----QDFIDVIKIFIDNLDPNKLFVNIKSNNO 1140  
Qy 655 -----EAFQGNFIISEIRPSEELSPELIKSDAWGSGGTWISGNSLAINSVNGTFR 707  
Db 1141 TTDSITLNOQYFFKFKLN-LBPKLIF--DLIKN-----LINSPIKLVNDKKNKIK 1188  
Qy 708 ---QNTLSGASYTS-----MNP-----NNGPGKVIRMSREAVPERSY 744  
Db 1189 IESNKAKIKISILITSVNIPENSMLMNFENNQLSQLPSSIDLFXNLNLSNOQRLNFAKAI 1248  
Qy 745 LQSSSKYISEKFTTTNN 762  
Db 1249 VELNK---EKLSNLIN 1263

Search completed: May 15, 2006, 20:44:04  
Job time : 49 secs



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QY 364 DSIATLVKYOAKLKHNYQIDKDSLSEIYVGDIDKLLCPDQSEQMYTNNKIAFENEYITK 423
D 365 DSMIVLAKYQAKLKQDQVQDKDSLSEIYVGDIDKLLCPDQSEQIYTNINIAFENEYITK 424
QY 424 IAFKKLNSLRVEVTANFYDSSTGDIIDLNKKKIESSAEPSMLNANDGVYMPIGTSET 483
D 425 LTFKKKNSLRVEVTANFYDSSTGDMIDLNKKKIESSAEPSMLNANDGVYMPIGTSET 484
QY 484 FLTPINGFLVVDNSRLVLTCKSYLRETLATDLSNKEKTLVPPNGFISNIIVENG 543
D 485 FLTPINGFLVVDNSRLVLTCKSYLRETLATDLSNKEKTLVPPNGFISNIIVENG 544
QY 544 EGENLEPMKANNKAAVYDHGTGCVNGTKVLYVHEDGESQFIQDKLKTETVYIYVKG 603
D 545 EGENLEPMKANNKAAVYDHGTGCVNGTKVLYVHEDGESQFIQDKLKTETVYIYVKG 604
QY 604 AAIYLDKDKNGDYIYEETNNLEDFQAVTKRFTIGTDSRVHLIPTSQNGEBAFGNFI 663
D 605 AAIYLDKDKNGDYIYEETNNLEDFQAVTKRFTIGTDSRVHLIPTSQNGEBAFGNFI 664
QY 664 SEIRPSEBLSPELIKSDAWGSGGTWISGNSLINSNVNGTFRQNLSESYSTYSMNFN 723
D 665 SEIRPSEBLSPELIKSDAWGSGGTWISGNSLINSNVNGTFRQNLSESYSTYSMNFN 724
QY 724 VNGGKATYINSREVFERSYLOFSSKYISEKFTTTNTGTYEELSRASRGVINFQDF 783
D 725 ITGGKATYINSREVFERSYLOFSSKYISEKFTTTNTGTYEELSRASRGVINFQDF 784
QY 784 SIK 786
D 785 SIK 787
```

## RESULT 2

```
Q5JZ20_BACTU PRELIMINARY; PRT; 788 AA.
ID Q5JZ20_BACTU PRELIMINARY; PRT; 788 AA.
AC Q5JZ20;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE 1ap3a protein.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OC NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Van Rie J., Arnaut G., Boets A., Damme N.;
RT "Gene encoding insecticidal secreted proteins from Bacillus thuringiensis."
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ872070; CA143275.1; -; Genomic_DNA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0016941; F:oxidoreductase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR003305; CBM Cenc.
DR Pfam; PF02018; CBM_4_9; I.
KW Oxidoreductase.
SQ SEQUENCE 788 AA; 88037 MW; 5A7314AA1DA6088 CRC64;
```

Query Match 81.2%; Score 3243.5; DB 2; Length 788;  
Best Local Similarity 80.9%; Pred. No. 1.2e-143;  
Matches 634; Conservative 65; Mismatches 84; Indels 1; Gaps 1;

```
QY 4 NTKLSVTAALPSFIDYFNGIYGFATGIDIMNMIFKTTGTGDLTLDLILKNOQLINISGK 63
D 5 NTKLSVTAALPSFIDYFNGIYGFATGIDIMNMIFKTTGTGDLTLDLILKNOQLINISGK 64
QY 64 LDGNGSLNDLILKNOQLINISGK 123
D 65 LDGNGSLNDLILKNOQLINISGK 124
```

```
QY 124 LSDVMKQNYALGQIEYLSKOLKEISDKLDVINNVNLINLTETIPAYORIKYVNEKFE 183
D 125 LSDVMKQNYALGQIEYLSKOLKEISDKLDVINNVNLINLTETIPAYORIKYVNEKFE 184
QY 184 ALTSATETNLKTYQDSSHDHIDELTELFLASVTGNVDGEFYLNTFHDVWIGNLF 243
D 185 ELTFATETNLKTYQDSSHDHIDELTELFLASVTGNVDGEFYLNTFHDVWIGNLF 244
QY 244 GRSALKTASELAKENLKTSGSEGVNPNLYLTLTQAAPFLTLTCRLGLGADIDYT 303
D 245 GRSALKTASELAKENLKTSGSEGVNPNLYLTLTQAAPFLTLTCRLGLGADIDYT 304
QY 304 PINNEHLNKEKEFRVNIPTLSNTFSNPYERARSGDXAKITMEAKPGYALVGEPIK 363
D 305 PINNEHLNKEKEFRVNIPTLSNTFSNPYERARSGDXAKITMEAKPGYALVGEPIK 364
QY 364 DSIATLVKYOAKLKHNYQIDKDSLSEIYVGDIDKLLCPDQSEQMYTNNKIAFENEYITK 423
D 365 DSIATLVKYOAKLKHNYQIDKDSLSEIYVGDIDKLLCPDQSEQIYTNINIAFENEYITK 424
QY 424 IAFKKLNSLRVEVTANFYDSSTGDIIDLNKKKIESSAEPSMLNANDGVYMPIGTSET 483
D 425 IAFKKLNSLRVEVTANFYDSSTGDIIDLNKKKIESSAEPSMLNANDGVYMPIGTSET 484
QY 484 FLTPINGFLVVDNSRLVLTCKSYLRETLATDLSNKEKTLVPPNGFISNIIVENG 543
D 485 FLTPINGFLVVDNSRLVLTCKSYLRETLATDLSNKEKTLVPPNGFISNIIVENG 544
QY 544 EGENLEPMKANNKAAVYDHGTGCVNGTKVLYVHEDGESQFIQDKLKTETVYIYVKG 603
D 545 EGENLEPMKANNKAAVYDHGTGCVNGTKVLYVHEDGESQFIQDKLKTETVYIYVKG 604
QY 604 AAIYLDKDKNGDYIYEETNNLEDFQAVTKRFTIGTDSRVHLIPTSQNGEBAFGNFI 663
D 605 AAIYLDKDKNGDYIYEETNNLEDFQAVTKRFTIGTDSRVHLIPTSQNGEBAFGNFI 664
QY 664 SEIRPSEBLSPELIKSDAWGSGGTWISGNSLINSNVNGTFRQNLSESYSTYSMNFN 723
D 665 SEIRPSEBLSPELIKSDAWGSGGTWISGNSLINSNVNGTFRQNLSESYSTYSMNFN 724
QY 724 VNGGKATYINSREVFERSYLOFSSKYISEKFTTTNTGTYEELSRASRGVINFQDF 782
D 725 VNGGKATYINSREVFERSYLOFSSKYISEKFTTTNTGTYEELSRASRGVINFQDF 784
QY 783 SIK 786
D 785 SIK 788
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## RESULT 3

```
Q58I33_BACTU PRELIMINARY; PRT; 789 AA.
ID Q58I33_BACTU PRELIMINARY; PRT; 789 AA.
AC Q58I33;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE Vegetative insecticidal protein.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OC NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cai J., Xiao L.;
RT "Bacillus thuringiensis strain 9816C vegetative insecticidal protein gene."
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY945939; AA949395.1; -; Genomic_DNA.
KW Oxidoreductase.
SQ SEQUENCE 789 AA; 88675 MW; 9F13448BAE7C7AA CRC64;
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Query Match 79.5%; Score 3176.5; DB 2; Length 789;



Best Local Similarity 78.6%; Pred. No. 1.7e-140;  
Matches 621; Conservative 70; Mismatches 94; Indels 5; Gaps 3;

```

OY 1 MOKNN-KLSVKALPSFIDYFNGIYGATGICDIIIMMIFKTMNGDUTLDEILKNOQLNE 59
DB 1 MOKNNKTLSTRALPSFIDYFNGIYGATGICDIIIMMIFKTMNGDUTLDEILKNOQLNE 60
OY 60 ISGKLDGVNGSLNDLIAQGNLDTLSKEILKIANEQNKVLDNVTKLDAINIMLNTYLPK 119
DB 61 ISGKLDGVNGSLNDLIAQGNLDTLSKEILKIANEQNKVLDNVTKLDAINIMLNTYLPK 120
OY 120 ITSMUSDVWKQNYALGLQIEYLSKQIKESIDKLDVINNVNLINSTLITTPAYQRIKYVN 179
DB 121 ITSMUSDVWKQNYALGLQIEYLSKQIKESIDKLDVINNVNLINSTLITTPAYQRIKYVN 180
OY 180 EKFEALTSATETNLTCKDSSHTDILDELTELTELAKSVTKNDVGFEEYNTFHDVWG 239
DB 181 EKFEALTSATETNLTCKDSSHTDILDELTELTELAKSVTKNDVGFEEYNTFHDVWG 240
OY 240 NNLFGRSALKTASSELIAKENLKTSGSEVGNVNFILVLTALQAKAFLLTTCRKLGLAD 299
DB 241 NNLFGRSALKTASSELITKENVKTSGSEVGNVNFILVLTALQAKAFLLTTCRKLGLAD 300
OY 300 IDYTPINMEHLNKEKEEPRVNIPLTSLNTPSNPTEKARGSDKAKIIMEARPGYALVGF 359
DB 301 IDYTPINMEHLNKEKEEPRVNIPLTSLNTPSNPTEKARGSDKAKIIMEARPGYALVGF 360
OY 360 EISKOSIAVLKYQAKLKHNYOIDKDSISEIYVGDIDKLLCPDQSEOMYTNKIAFPREX 419
DB 361 EISNDSTIVLKYQAKLKHNYOIDKDSISEIYVGDIDKLLCPDQSEOMYTNKIAFPREX 420
OY 420 VITKIDFTKKNKTLARIEVTANFYDSSTGIDIDANKKIESSSEAFSEMLNANDGVYMPIGT 479
DB 421 VITKIDFTKKNKTLARIEVTANFYDSSTGIDIDANKKIESSSEAFSEMLNANDGVYMPIGT 480
OY 480 ISEFTPLTPINGFGLVVDENSRLVLTJCKSYLREFTLLATDLSNKEKTLIVPPNGFISNIVE 539
DB 481 ISEFTPLTPINGFGLVVDENSRLVLTJCKSYLREFTLLATDLSNKEKTLIVPPNGFISNIVE 540
OY 540 NGNLEGENLEBPKANNKNAAYVDHTGCVNGTKVLYHDEGEPSQFIDGDKLKTETVYIYI 599
DB 541 NGNLEGENLEBPKANNKNAAYVDHTGCVNGTKVLYHDEGEPSQFIDGDKLKTETVYIYI 600
OY 600 VKGKAIVLYLDEKNGDIYIEETNNLEDPQAVTKAFITGDSRVAHLIFTSONGEBAFGG 659
DB 601 VKGKPSIHLKDENGDIYIEEDTNNLEDPQAVTKAFITGDSRVAHLIFTSONGEBAFGG 660
OY 660 NFIISEIRPSEBELLSPELIKSDAVVSGQGTWISGNSLINSNVNGTFRQNTSLSEYSTYS 719
DB 661 NFIISEIRPSEBELLSPELIKSDAVVSGQGTWISGNSLINSNVNGTFRQNTSLSEYSTYS 720
OY 720 MNFVNGGKVTIINSREVPERSRVLOFSSKYSISEKFTTTNNNGLYVELSRAS--RG 776
DB 721 VYFVSQGANVRIRNSREVLPEKRYMS-GADVSEMFTTKEKQNFYIELSQNNLYGCP 779
OY 777 VINFGDFSIRK 786
DB 780 IVHFYDVSIK 789

```

RP NUCLEOTIDE SEQUENCE.  
RC STRAIN-WY-197;  
RA Li J., Yan J., Yuan Z.;  
RT "Cloning and expression of vip3A gene from *Bacillus thuringiensis*  
RT strain WY-197."  
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY743436; AAU89707.1; -; Genomic DNA.  
DR GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR003305; CEM\_CenC.  
DR Pfam; PF02018; CEM\_4\_9; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 789 AA; 88642 MW; 6322FD4A4EBCT0D4 CRC64;

Query Match 79.5%; Score 3175.5; DB 2; Length 789;  
Best Local Similarity 78.6%; Pred. No. 1.8e-140;  
Matches 621; Conservative 70; Mismatches 94; Indels 5; Gaps 3;

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OY 1 MOKNN-KLSVKALPSFIDYFNGIYGATGICDIIIMMIFKTMNGDUTLDEILKNOQLNE 59
DB 1 MOKNNKTLSTRALPSFIDYFNGIYGATGICDIIIMMIFKTMNGDUTLDEILKNOQLNE 60
OY 60 ISGKLDGVNGSLNDLIAQGNLDTLSKEILKIANEQNKVLDNVTKLDAINIMLNTYLPK 119
DB 61 ISGKLDGVNGSLNDLIAQGNLDTLSKEILKIANEQNKVLDNVTKLDAINIMLNTYLPK 120
OY 120 ITSMUSDVWKQNYALGLQIEYLSKQIKESIDKLDVINNVNLINSTLITTPAYQRIKYVN 179
DB 121 ITSMUSDVWKQNYALGLQIEYLSKQIKESIDKLDVINNVNLINSTLITTPAYQRIKYVN 180
OY 180 EKFEALTSATETNLTCKDSSHTDILDELTELTELAKSVTKNDVGFEEYNTFHDVWG 239
DB 181 EKFEALTSATETNLTCKDSSHTDILDELTELTELAKSVTKNDVGFEEYNTFHDVWG 240
OY 240 NNLFGRSALKTASSELIAKENLKTSGSEVGNVNFILVLTALQAKAFLLTTCRKLGLAD 299
DB 241 NNLFGRSALKTASSELITKENVKTSGSEVGNVNFILVLTALQAKAFLLTTCRKLGLAD 300
OY 300 IDYTPINMEHLNKEKEEPRVNIPLTSLNTPSNPTEKARGSDKAKIIMEARPGYALVGF 359
DB 301 IDYTPINMEHLNKEKEEPRVNIPLTSLNTPSNPTEKARGSDKAKIIMEARPGYALVGF 360
OY 360 EISKOSIAVLKYQAKLKHNYOIDKDSISEIYVGDIDKLLCPDQSEOMYTNKIAFPREX 419
DB 361 EISNDSTIVLKYQAKLKHNYOIDKDSISEIYVGDIDKLLCPDQSEOMYTNKIAFPREX 420
OY 420 VITKIDFTKKNKTLARIEVTANFYDSSTGIDIDANKKIESSSEAFSEMLNANDGVYMPIGT 479
DB 421 VITKIDFTKKNKTLARIEVTANFYDSSTGIDIDANKKIESSSEAFSEMLNANDGVYMPIGT 480
OY 480 ISEFTPLTPINGFGLVVDENSRLVLTJCKSYLREFTLLATDLSNKEKTLIVPPNGFISNIVE 539
DB 481 ISEFTPLTPINGFGLVVDENSRLVLTJCKSYLREFTLLATDLSNKEKTLIVPPNGFISNIVE 540
OY 540 NGNLEGENLEBPKANNKNAAYVDHTGCVNGTKVLYHDEGEPSQFIDGDKLKTETVYIYI 599
DB 541 NGNLEGENLEBPKANNKNAAYVDHTGCVNGTKVLYHDEGEPSQFIDGDKLKTETVYIYI 600
OY 600 VKGKAIVLYLDEKNGDIYIEETNNLEDPQAVTKAFITGDSRVAHLIFTSONGEBAFGG 659
DB 601 VKGKPSIHLKDENGDIYIEEDTNNLEDPQAVTKAFITGDSRVAHLIFTSONGEBAFGG 660
OY 660 NFIISEIRPSEBELLSPELIKSDAVVSGQGTWISGNSLINSNVNGTFRQNTSLSEYSTYS 719
DB 661 NFIISEIRPSEBELLSPELIKSDAVVSGQGTWISGNSLINSNVNGTFRQNTSLSEYSTYS 720
OY 720 MNFVNGGKVTIINSREVPERSRVLOFSSKYSISEKFTTTNNNGLYVELSRAS--RG 776
DB 721 VYFVSQGANVRIRNSREVLPEKRYMS-GADVSEMFTTKEKQNFYIELSQNNLYGCP 779
OY 777 VINFGDFSIRK 786
DB 780 IVHFYDVSIK 789

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Db 780 IVHFYDVSIR 789

## RESULT 5

Q99SG2\_BACTU PRELIMINARY; PRT; 789 AA.

AC Q99SG2;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Vegetative insecticidal protein.  
GN Name=vip3;  
OS Bacillus thuringiensis serovar lewis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=169759;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=YBT-833;  
RA Cai Q., Liu Z., Sun M., Yu Z.;  
RT "Vegetative insecticidal protein gene vip3 from Bacillus thuringiensis serovar lewis strain YBT-833."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY044227; AK95326.1; -; Genomic DNA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR InterPro; IPR003305; CBM\_Cenc.  
DR Pfam; PF02018; CBM\_4\_9; I.  
KM Oxidoreductase.  
SQ SEQUENCE 789 AA; 88671 MM; 9DD746486823C7AE CRC64;

Query Match 79.5%; Score 3175.5; DB 2; Length 789;  
Best Local Similarity 78.6%; Pred. No. 1.8e-140;  
Matches 621; Conservative 70; Mismatches 94; Indels 5; Gaps 3;

QY 1 MOKNN-ELSYKALPSFIDYNGYGFATGKIDIMNMFKNTGSDLLDELKQOOLNE 59  
DB 1 MNKNNTSTRALPSFIDYNGYGFATGKIDIMNMFKNTGSDLLDELKQOOLNE 60  
QY 60 ISGKLDSVNSLNDLDAQNLDELTELSEIKIANEQNKVINDVTKLDAINLMNTYLPK 119  
DB 61 ISGKLDSVNSLNDLDAQNLDELTELSEIKIANEQNKVINDVTKLDAINLMNTYLPK 120  
QY 120 ITSMLSVVKONTALGQIETLSKQKEISDKLDVINNVNLINSTLETTPAYORIKYVN 179  
DB 121 ITSMLSVVKONTALGQIETLSKQKEISDKLDVINNVNLINSTLETTPAYORIKYVN 180  
QY 180 EKPEALTSATETNLTQKQDSHNDIIDELEIETELASVTKNDVGEFEYLNTHFDWMIG 239  
DB 181 EKPEALTSATETNLTQKQDSHNDIIDELEIETELASVTKNDVGEFEYLNTHFDWMIG 240  
QY 240 NNLFGSALXTASSELAKENILKTSSEVGVNVPYLVLTALQAKAFLLTTCRKLGLAD 299  
DB 241 NNLFGSALXTASSELAKENILKTSSEVGVNVPYLVLTALQAKAFLLTTCRKLGLAD 300  
QY 300 IDYTPINNEHLNKEKEFRVNIILPTLNTSNPNYEAKSGSDKDAKIMEAKGEYALVGF 359  
DB 301 IDYTPINNEHLNKEKEFRVNIILPTLNTSNPNYEAKSGSDKDAKIMEAKGEYALVGF 360  
QY 360 EISKDSIAVLKVVQAKLKHNYQIDKDSLRIYVGDIDKLCPPDSEOMYTNKAPPNEX 419  
DB 361 EISKDSIAVLKVVQAKLKHNYQIDKDSLRIYVGDIDKLCPPDSEOMYTNKAPPNEX 420  
QY 420 VITKIAFTKLKLSLRYEVNTANFYDSTGDIIDLNKKKLESSEAEFSMANNNDGVYMPIGT 479  
DB 421 VITKIDFTKLMKTLRYEVNTANFYDSTGDIIDLNKKKLESSEAEFSMANNNDGVYMPIGT 480  
QY 480 ISSTFLTPINGFGLVVDNSRLVTLTKSKYSIRETLATDLSNKETKLIIVPENGFSINIVE 539  
DB 481 ISSTFLTPINGFGLVVDNSRLVTLTKSKYSIRETLATDLSNKETKLIIVPENGFSINIVE 540  
QY 540 NGNLEGENLEPMWANNKQAVVDHTGVNGTKVLVYHEDGEFSQPIGKCLKKTEYVVOYI 599  
DB 541 NGNLEGENLEPMWANNKQAVVDHTGVNGTKVLVYHEDGEFSQPIGKCLKKTEYVVOYI 600

QY 600 VKGKAAYLKDEKNGDYIEETINNELEDFOAVTKRFTTGTSSRVHLIFTSNGEAEFGC 659  
DB 601 VKGKPSHLKDEKNGDYIEETINNELEDFOAVTKRFTTGTGTDLKGVYLLKSGDEAMGD 660  
QY 660 NFIISIRPSEELLSPELIKSDAMVSGQGTWISGNSLINSVNGTFRRQLSLSEYSTYS 719  
DB 661 NFIILSIRPSEELLSPELINTNMWSTGTSINISGNTLTYQGGRGILKQMLQDSFSTYR 720  
QY 720 MNFNNGVFGKVTIRNSREVVEERSYLOFSKYSSEKFTTTNTGUYVELSRASS--RG 776  
DB 721 VYFVSQDANVRIRNSREVVEERSYLOFSKYSSEKFTTTNTGUYVELSRASS--RG 779  
QY 777 VINFGDFSIR 786  
DB 780 IVHFYDVSIR 789

## RESULT 6

Q938Z1\_BACTU PRELIMINARY; PRT; 789 AA.

ID Q938Z1\_BACTU PRELIMINARY;  
AC Q938Z1\_O8L2N0;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Vegetative insecticidal protein Vip3A (Vegetative insecticidal protein vip3v).  
GN Name=vip3A; Synonyms=vip3A-WB5, vip3v;  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=SI01, and 611;  
RA Chen J., Yu J., Pang Y., Tang L.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Wu Y., Guan X.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=WB 50;  
RX PubMed=15604775; DOI=10.1023/B:BILE.0000045645.45536.3f;  
RA Xu Z.L., Guo W.Y., Qiu J.Z., Huang T.P., Li X.B., Guan X.;  
RT "Cloning and localization of vip3A gene of Bacillus thuringiensis.";  
RL Biotechnol. Lett. 26:1425-1428 (2004).  
RN [4]

RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=2244722; PubMed=12356474; DOI=10.1016/S1046-5928(02)00515-6;  
RA Does V.A., Anup Kumar K., Jayakumar R., Sekar V.;  
RT "Cloning and expression of the vegetative insecticidal protein (vip3v) gene of Bacillus thuringiensis in Escherichia coli.";  
RL Protein Expr. Purif. 26:82-88 (2002).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C9;  
RA Liu R., Song F., Zhang J.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY074707; AAL69543.1; -; Genomic DNA.  
DR EMBL; AF500478; AAM22456.2; -; Genomic DNA.  
DR EMBL; AF295778; AAP51131.1; -; Genomic DNA.  
DR EMBL; AF373030; AAN60738.1; -; Genomic DNA.  
DR EMBL; AY489126; AAR36859.1; -; Genomic DNA.  
DR EMBL; AY074708; AAL69544.1; -; Genomic DNA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR InterPro; IPR003305; Cenc\_carb\_bd.  
DR Pfam; PF02018; CBM\_4\_9; I.  
KM Oxidoreductase.  
SQ SEQUENCE 789 AA; 88672 MM; 9DD746486823C7AE CRC64;

Query Match 79.5%; Score 3175.5; DB 2; Length 789;

Best Local Similarity 78.6%; Pred. No. 1.8e-140;  
Matches 621; Conservative 70; Mismatches 94; Indels 5; Gaps 3;

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QY 1 MOKN-KLSVKALPSFIDYFNGIYGPATGICDINMMIFPTNGGDLTLEILLKNOQLNE 59
DB 1 MKNKNTKSTRALPSFIDYFNGIYGPATGICDINMMIFPTNGGDLTLEILLKNOQLNE 60
QY 60 ISGKLDGVNGSLNDLLAOGNLTDELTELSKEILKIANEQNVLDVNNKLDALINMLRYLPK 119
DB 61 ISGKLDGVNGSLNDLLAOGNLTDELTELSKEILKIANEQNVLDVNNKLDALINMLRYLPK 120
QY 120 ITSMLSDVWKONVYALGLQIEYLSKQLEISDKLDVINNVVLIINSTLTETTPAYQRIKYVN 179
DB 121 ITSMLSDVWKONVYALGLQIEYLSKQLEISDKLDVINNVVLIINSTLTETTPAYQRIKYVN 180
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DB 181 EKFEALTATETNLTCKODSSHDTLDLDELTELAKSVTKNDVDGFEFYLTFFHDVWG 240
QY 240 NNLFGRSALKTASBLIAKENLKTSGSEGVNVPFLIVLTALQAKAFLLTTCKRLGLAD 299
DB 241 NNLFGRSALKTASBLIAKENLKTSGSEGVNVPFLIVLTALQAKAFLLTTCKRLGLAD 300
QY 300 IYTPIMNEHLNKEKEEPRVNIPLTSTFSPNPNYKARAGSDAKIIMEAKPGYALVGF 359
DB 301 IYTPIMNEHLNKEKEEPRVNIPLTSTFSPNPNYKARAGSDAKIIMEAKPGYALVGF 360
QY 360 EISKDSIALVKYQAKLKHNOIQIDKOSLSEIYVGDIDKLLCPDQSEQMTYTNKIAFPNEY 419
DB 361 EISKDSIALVKYQAKLKHNOIQIDKOSLSEIYVGDIDKLLCPDQSEQMTYTNKIAFPNEY 420
QY 420 VITKIAFTKCLNSLRKYEVYANFYDSSTGDIIDLNKKKIESSEAFSMANNDGVMPYIGT 479
DB 421 VITKIDFTKCKMTLRKYEVYANFYDSSTGDIIDLNKKKIESSEAFSMANNDGVMPYIGT 480
QY 480 ISETFLTPINGGLVVDENSRLVTLTCKSYLRETLATDLSNKETKLIIPPNGFISNIYE 539
DB 481 ISETFLTPINGGLVVDENSRLVTLTCKSYLRETLATDLSNKETKLIIPPNGFISNIYE 540
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DB 541 NGNLEGENLEPMKANNKNAVYDHTGVNGTGYLVLYHEDGEPGQFIDKDKLKTREYVIOYT 600
QY 600 VKGKAALYLDKDEKNGDIYEETNNLEDPQAVTKKPFITGDSRVHLIFTSONGEBAFG 659
DB 601 VKGKSIHLKDEKNGDIYEETNNLEDPQAVTKKPFITGDSRVHLIFTSONGEBAFG 660
QY 660 NFIISEIRPSEELLSPBLIKSDAWGSGQTWISGNSLININSVNGTFRONTLSLESYSTYS 719
DB 661 NFIISEIRPSEELLSPBLIKSDAWGSGQTWISGNSLININSVNGTFRONTLSLESYSTYS 720
QY 720 MNFVNGFGKTYTIRNSREVFERSYLOPSSRYISEKFTTTNTNGLYVLSRASS--RG 776
DB 721 VYFVSQGANVRIRNSREVLFEKRYMS-GAKDVSEMTTKPEKONFYELSGNNLYGCP 779
QY 777 VINFGDPSIK 786
DB 780 IVHFYDVSIK 789

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RESULT 7  
Q58X12\_BACTU PRELIMINARY; PRT: 789 AA.  
AC Q58X12-  
DT 10-MAY-2005 (TREMBLrel. 30, Created)  
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
DE Vegetative insecticidal protein.  
GN Name=vi33JB;  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
NCBI\_TaxID=1428;

RN [1]  
RA NUCLEOTIDE SEQUENCE.  
RP Abdelkefi Mestari L., Tounsi S., Jaoua S.;  
RT "Characterization of a novel vip3-type gene from Bacillus  
RT thuringiensis and evidence of its presence on a large plasmid";  
RL FEMS Microbiol. Lett. 244:353-358 (2005).  
DR EMBL; AY739665; AA065132.1; -; Genomic\_DNA.  
KW Oxidoreductase.  
SQ SEQUENCE 789 AA; 88671 MW; EC5355939F6CA CRC64;

Query Match 79.4%; Score 3173.5; DB 2; Length 789;  
Best Local Similarity 78.5%; Pred. No. 2.3e-140;  
Matches 620; Conservative 71; Mismatches 94; Indels 5; Gaps 3;

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QY 1 MOKN-KLSVKALPSFIDYFNGIYGPATGICDINMMIFPTNGGDLTLEILLKNOQLNE 59
DB 1 MKNKNTKSTRALPSFIDYFNGIYGPATGICDINMMIFPTNGGDLTLEILLKNOQLNE 60
QY 60 ISGKLDGVNGSLNDLLAOGNLTDELTELSKEILKIANEQNVLDVNNKLDALINMLRYLPK 119
DB 61 ISGKLDGVNGSLNDLLAOGNLTDELTELSKEILKIANEQNVLDVNNKLDALINMLRYLPK 120
QY 120 ITSMLSDVWKONVYALGLQIEYLSKQLEISDKLDVINNVVLIINSTLTETTPAYQRIKYVN 179
DB 121 ITSMLSDVWKONVYALGLQIEYLSKQLEISDKLDVINNVVLIINSTLTETTPAYQRIKYVN 180
QY 180 EKFEALTATETNLTCKODSSHDTLDLDELTELAKSVTKNDVDGFEFYLTFFHDVWG 239
DB 181 EKFEALTATETNLTCKODSSHDTLDLDELTELAKSVTKNDVDGFEFYLTFFHDVWG 240
QY 240 NNLFGRSALKTASBLIAKENLKTSGSEGVNVPFLIVLTALQAKAFLLTTCKRLGLAD 299
DB 241 NNLFGRSALKTASBLIAKENLKTSGSEGVNVPFLIVLTALQAKAFLLTTCKRLGLAD 300
QY 300 IYTPIMNEHLNKEKEEPRVNIPLTSTFSPNPNYKARAGSDAKIIMEAKPGYALVGF 359
DB 301 IYTPIMNEHLNKEKEEPRVNIPLTSTFSPNPNYKARAGSDAKIIMEAKPGYALVGF 360
QY 360 EISKDSIALVKYQAKLKHNOIQIDKOSLSEIYVGDIDKLLCPDQSEQMTYTNKIAFPNEY 419
DB 361 EISKDSIALVKYQAKLKHNOIQIDKOSLSEIYVGDIDKLLCPDQSEQMTYTNKIAFPNEY 420
QY 420 VITKIAFTKCLNSLRKYEVYANFYDSSTGDIIDLNKKKIESSEAFSMANNDGVMPYIGT 479
DB 421 VITKIDFTKCKMTLRKYEVYANFYDSSTGDIIDLNKKKIESSEAFSMANNDGVMPYIGT 480
QY 480 ISETFLTPINGGLVVDENSRLVTLTCKSYLRETLATDLSNKETKLIIPPNGFISNIYE 539
DB 481 ISETFLTPINGGLVVDENSRLVTLTCKSYLRETLATDLSNKETKLIIPPNGFISNIYE 540
QY 540 NGNLEGENLEPMKANNKNAVYDHTGVNGTGYLVLYHEDGEPGQFIDKDKLKTREYVIOYT 599
DB 541 NGNLEGENLEPMKANNKNAVYDHTGVNGTGYLVLYHEDGEPGQFIDKDKLKTREYVIOYT 600
QY 600 VKGKAALYLDKDEKNGDIYEETNNLEDPQAVTKKPFITGDSRVHLIFTSONGEBAFG 659
DB 601 VKGKSIHLKDEKNGDIYEETNNLEDPQAVTKKPFITGDSRVHLIFTSONGEBAFG 660
QY 660 NFIISEIRPSEELLSPBLIKSDAWGSGQTWISGNSLININSVNGTFRONTLSLESYSTYS 719
DB 661 NFIISEIRPSEELLSPBLIKSDAWGSGQTWISGNSLININSVNGTFRONTLSLESYSTYS 720
QY 720 MNFVNGFGKTYTIRNSREVFERSYLOPSSRYISEKFTTTNTNGLYVLSRASS--RG 776
DB 721 VYFVSQGANVRIRNSREVLFEKRYMS-GAKDVSEMTTKPEKONFYELSGNNLYGCP 779
QY 777 VINFGDPSIK 786
DB 780 IVHFYDVSIK 789

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RESULT 8  
Q45792\_BACTU

ID Q45792\_BACTU PRELIMINARY; PRT; 789 AA.  
AC Q45792;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Vlp3A(A) protein.  
GN Name=Vlp3A(a);  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=AB88;  
RX MEDLINE=96224295; PubMed=8643585; DOI=10.1073/pnas.93.11.5389;  
RA Eernuch J.J., Warren G.W., Mullins M.A., Nye G.J., Craig J.A.,  
Koriel M.G.;  
RT "Vlp3A, a novel Bacillus thuringiensis vegetative insecticidal protein  
with a wide spectrum of activities against lepidopteran insects.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:5389-5394(1996).  
DR EMBL: L48811; AAC37036.1; -; Genomic DNA.  
DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
DR InterPro: IPR003305; CMC\_Cenc.  
DR Pfam: PF02018; CMC\_4\_9; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 789 AA; 88671 MW; 9DD3DD926823C7AE CRC64;

Query Match 79.4%; Score 3171.5; DB 2; Length 789;  
Best Local Similarity 78.5%; Pred. No. 2.8e-140;  
Matches 620; Conservative 71; Mismatches 94; Indels 5; Gaps 3;

QY 1 MOKNN-KLSVYALPSFIDYFNGIYGFATGIDINMMIFKNTGDLTDLIELKNQOOLNE 59  
DB 1 MNKNNTKSTRALPSFIDYFNGIYGFATGIDINMMIFKNTGDLTDLIELKNQOOLND 60  
QY 60 ISGKLDGVNSGLDLAOGNLDTELSEIKIANEQKQVNDVNTKDAINMLNTYLPK 119  
DB 61 ISGKLDGVNSGLDLAOGNLDTELSEIKIANEQKQVNDVNTKDAINMLNTYLPK 120  
QY 120 ITSMUSDVMKONVALSGOIEYLSKOLKEISDKLDVINNVNLINSTLEITPAVORIKYVN 179  
DB 121 ITSMUSDVMKONVALSGOIEYLSKOLKEISDKLDVINNVNLINSTLEITPAVORIKYVN 180  
QY 180 EKFPALTSATEPNTKTKODSSHTDILDELTELTELAKSVTKNDVGEFFYNTFHDVWG 239  
DB 181 EKFPALTSATEPNTKTKODSSHTDILDELTELTELAKSVTKNDVGEFFYNTFHDVWG 240  
QY 240 NNLFGRSALKTASSELIAKENIKTSGEVGVNYYNPLIVFALQAKAFPLTTCRKLGIAD 299  
DB 241 NNLFGRSALKTASSELIAKENIKTSGEVGVNYYNPLIVFALQAKAFPLTTCRKLGIAD 300  
QY 300 IDYPIPMNEHLNKKKEEPRVNIILPLTSFTSPNPKYKRGSKDAKIMKAPGVALYGF 359  
DB 301 IDYPIPMNEHLNKKKEEPRVNIILPLTSFTSPNPKYKRGSKDAKIMKAPGVALYGF 360  
QY 360 EISKDSIAVLKYVQAUKHANYQIDKDSISEIYVGDIDELCPDSEQMYNTNKAIFPNEX 419  
DB 361 EISKDSIAVLKYVQAUKHANYQIDKDSISEIYVGDIDELCPDSEQMYNTNKAIFPNEX 420  
QY 420 VITKIAFLPKANLSLREYVNTANFYDSSITDIDLNKKKISSSAEFSMLNANDGYMPYIGT 479  
DB 421 VITKIDFTKMKTKTAREYVNTANFYDSSITDIDLNKKKISSSAEFSMLNANDGYMPYIGT 480  
QY 480 ISEFLFPIFGFGLVVDENSRLLVLTCKSYLRETLTADLSNKKETKLVPPNGFISNIVE 539  
DB 481 ISEFLFPIFGFGLVVDENSRLLVLTCKSYLRETLTADLSNKKETKLVPPNGFISNIVE 540  
QY 540 NGNLEGENLEBPWKANNKNAAYVDHTGVNGTIVLYVHEDEFSQFIDGKLKLTETEVLYQYI 599  
DB 541 NGNLEGENLEBPWKANNKNAAYVDHTGVNGTIVLYVHEDEFSQFIDGKLKLTETEVLYQYI 600  
QY 600 VKGKAATYLDKDKGDIYIEETNNELEPQAVTKRFTITGDSRVHLIFTSQNGBEAFGG 659  
DB 600 VKGKAATYLDKDKGDIYIEETNNELEPQAVTKRFTITGDSRVHLIFTSQNGBEAFGG 659

DB 601 VKGKPSIHLKDNENTGYIHYEDTNNNLEDYQTIKRFITGDLKGVYLKKSQNGDEAMGD 660  
QY 660 NFIISEIRPSEBELSPELIKSDAVGSGTWISGNSINNSVNGTFRONLSIESYSTYS 719  
DB 661 NFIISEIRPSEBELSPELIKSDAVGSGTWISGNSINNSVNGTFRONLSIESYSTYS 720  
QY 720 MNFNVNGFGVYIRNSREVVFRSRYLOPSSKYSISEKFTTTNTGVLVELSRSS--RG 776  
DB 721 VYFVSQDANVRIKNSREVLFEKRYMS-GAKDVSEMTTTFEKNPFYIELSQNNLYGPF 779  
QY 777 VINFGDPSIK 786  
DB 780 IVHFPYDVSIK 789

## RESULT 9

Q8RS25\_BACTU PRELIMINARY; PRT; 789 AA.  
ID Q8RS25\_BACTU PRELIMINARY; PRT; 789 AA.  
AC Q8RS25;  
DT 01-JUN-2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)  
DE Vlp3A (Vlp184).  
GN Name=Vlp3A;  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=S184;  
RX MEDLINE=22744951; PubMed=12859763;  
RX DOI=10.1046/j.1365-2672.2003.01977.x;  
RA Chen J., Yu J., Tang L., Tang M., Shi Y., Pang Y.;  
RT "Comparison of the expression of Bacillus thuringiensis full-length  
and N-terminally truncated vlp3A gene in *Bacillus coli*.";  
RL J. Appl. Microbiol. 95:310-316(2003).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=S184;  
RX PubMed=12674638;  
RA Chen J.W., Tang L.X., Tang M.J., Shi Y.X., Pang Y.;  
RT "Cloning and expression product of vlp3A gene from Bacillus  
thuringiensis and analysis of insecticidal activity.";  
RL Sheng Wu Gong Cheng Xue Bao 18:687-692(2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Chen J., Yu J., Pang Y.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY074706; AA069542.1; -; Genomic DNA.  
DR EMBL: AY187679; AA032350.1; -; Genomic DNA.  
DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
DR InterPro: IPR003305; CMC\_Cenc.  
DR Pfam: PF02018; CMC\_4\_9; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 789 AA; 88645 MW; D9DF334011551472 CRC64;

Query Match 79.4%; Score 3171.5; DB 2; Length 789;  
Best Local Similarity 78.6%; Pred. No. 2.8e-140;  
Matches 621; Conservative 69; Mismatches 95; Indels 5; Gaps 3;

QY 1 MOKNN-KLSVYALPSFIDYFNGIYGFATGIDINMMIFKNTGDLTDLIELKNQOOLNE 59  
DB 1 MNKNNTKSTRALPSFIDYFNGIYGFATGIDINMMIFKNTGDLTDLIELKNQOOLND 60  
QY 60 ISGKLDGVNSGLDLAOGNLDTELSEIKIANEQKQVNDVNTKDAINMLNTYLPK 119  
DB 61 ISGKLDGVNSGLDLAOGNLDTELSEIKIANEQKQVNDVNTKDAINMLNTYLPK 120  
QY 120 ITSMUSDVMKONVALSGOIEYLSKOLKEISDKLDVINNVNLINSTLEITPAVORIKYVN 179  
DB 121 ITSMUSDVMKONVALSGOIEYLSKOLKEISDKLDVINNVNLINSTLEITPAVORIKYVN 180

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QY 180 EKFEALTSATEFNLTAKODSSHTDILDELTELTELAKSVTKNDVDGFEFYLTNTHDWMIG 239
DB 181 EKFEELTFATEITSSKVKDGSFPADILDELTELTELAKSVTKNDVDGFEFYLTNTHDWMIG 240
QY 240 NNLFGSALKTASELJAKENLTKTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLAD 299
DB 241 NNLFGSALKTASELJAKENLTKTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPIMNEHLNKEKEEFRRVNIPLTSLNTFSNPNYKARGSDKAKIMEAKGYALVGF 359
DB 301 IDYTSIMNEHLNKEKEEFRRVNIPLTSLNTFSNPNYKARGSDKAKIMEAKGYALVGF 360
QY 360 EISKSIAVLKYOAKLKHNYOIDKDSLEIYVGDIDLCPDQSEOMYTNKIAFPNEY 419
DB 361 EISNDSTVLKYEAQKONYQVDKDSLEVIYGMIDLCPDQSEQIYTNINNIYFPNEY 420
QY 420 VTTKIAFTKGLNSLRKYEVYANFPYDSGTGIDLNKKKISSSEAFSMLNANDGVYMPIGT 479
DB 421 VTTKIDFTKGMKTLREYVYANFPYDSGTGIDLNKKKISSSEAFSMLNANDGVYMPIGV 480
QY 480 ISETFLTPINGFGLVVDENSRLVTLTCKSYLRETLATDLNKKETKLIYPPNGFISNIVE 539
DB 481 ISETFLTPINGFGLVVDENSRLVTLTCKSYLRETLATDLNKKETKLIYPPNGFISNIVE 540
QY 540 NNLFGSALKTASELJAKENLTKTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLAD 299
DB 541 NNLFGSALKTASELJAKENLTKTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPIMNEHLNKEKEEFRRVNIPLTSLNTFSNPNYKARGSDKAKIMEAKGYALVGF 359
DB 301 IDYTSIMNEHLNKEKEEFRRVNIPLTSLNTFSNPNYKARGSDKAKIMEAKGYALVGF 360
QY 600 VKGKAALYKDEKNGDYIYEETNNLEBDFOAVTKRFTITGDSRVHLITFSONGEAFGG 659
DB 601 VKGKSIHLKDEKNGDYIYEETNNLEBDFOAVTKRFTITGDSRVHLITFSONGEAFGG 660
QY 660 NFIIEIRPSELLSPELIKSDAWYGSOGTWISGNSLINSNVNGTFRONLSLSYSTYS 719
DB 661 NFIIEIRPSELLSPELIKSDAWYGSOGTWISGNSLINSNVNGTFRONLSLSYSTYS 720
QY 720 MNFNVNGFGKVTIRNSREVVERSYLOFSSKYISEKFTTTTNNGTLYVHLSRASS--RG 776
DB 721 VYFSVSGDANVRIRNSREVLFEKRYMS-GAKDVSEMTTKPEKDNFYIELSGNNLYGCP 779
QY 777 VINFGDFSIRK 786
DB 780 IVHFYDVSIK 789

RESULT 10
069270_BACTU
ID 069270_BACTU PRELIMINARY; PRT; 789 AA.
AC 069270;
DT 01-AUG-1998 (Tremblrel. 07, last sequence update)
DT 01-AUG-1998 (Tremblrel. 07, last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, last annotation update)
DB Vegetative insecticidal protein.
GN Name=vip-8;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OC NCBI_TaxID=1428;
RX MEDLINE=21579339; PubMed=11722946;
RA Selvapandian A., Arora N., Rajagopal R., Jalali S.K., Venkatesan T.,
RT "Toxicity analysis of N- and C-terminus-deleted vegetative
RT insecticidal protein from Bacillus thuringiensis.",
RL Appl. Environ. Microbiol. 67:5855-5858(2001).
DR EMBL: Y17158; CAI:6665.1; -: Genomic DNA.
DR GO: GO:0016491; P:oxidoreductase activity; IEA.
DR InterPro: IPR003305; CMB_Cenc.
DR Pfam: PF02018; CMB_4_9; I.
KW Oxidoreductase.

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SQ SEQUENCE 789 AA; 88599 MW; 70619EA868237CAC CRC64;
Query Match 79 3%; Score 3168.5; DB 2; Length 789;
Best Local Similarity 78.5%; Pred. No.3.9e-140;
Matches 620; Conservative 70; Mismatches 95; Indels 5; Gaps 3;

QY 1 MOKNN-KLSVKALPFIDYFNIGIYFATGICIKIMNIPFTNTGDLTDEILKNOOLLNE 59
DB 1 MOKNNKTSTRALPFDIDFNIGIYFATGICIKIMNIPFTNTGDLTDEILKNOOLLNE 60
QY 60 ISGKLDGVNGSLINDLIAQGNLDTLSKEILKIANQONKYANDVNTKDALINMLNTYLPK 119
DB 61 ISGKLDGVNGSLINDLIAQGNLDTLSKEILKIANQONKYANDVNTKDALINMLNTYLPK 120
QY 120 ITSMISDVWKONYALGLQIEYLSKQLEISDGLDVYINNVVLIINSTLTETPYQRIKYVN 179
DB 121 ITSMISDVWKONYALGLQIEYLSKQLEISDGLDVYINNVVLIINSTLTETPYQRIKYVN 180
QY 180 EKFEALTSATEFNLTAKODSSHTDILDELTELTELAKSVTKNDVDGFEFYLTNTHDWMIG 239
DB 181 EKFEELTFATEITSSKVKDGSFPADILDELTELTELAKSVTKNDVDGFEFYLTNTHDWMIG 240
QY 240 NNLFGSALKTASELJAKENLTKTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLAD 299
DB 241 NNLFGSALKTASELJAKENLTKTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLAD 300
QY 300 IDYTPIMNEHLNKEKEEFRRVNIPLTSLNTFSNPNYKARGSDKAKIMEAKGYALVGF 359
DB 301 IDYTSIMNEHLNKEKEEFRRVNIPLTSLNTFSNPNYKARGSDKAKIMEAKGYALVGF 360
QY 360 EISKSIAVLKYOAKLKHNYOIDKDSLEIYVGDIDLCPDQSEOMYTNKIAFPNEY 419
DB 361 EISNDSTVLKYEAQKONYQVDKDSLEVIYGMIDLCPDQSEQIYTNINNIYFPNEY 420
QY 420 VTTKIAFTKGLNSLRKYEVYANFPYDSGTGIDLNKKKISSSEAFSMLNANDGVYMPIGT 479
DB 421 VTTKIDFTKGMKTLREYVYANFPYDSGTGIDLNKKKISSSEAFSMLNANDGVYMPIGV 480
QY 480 ISETFLTPINGFGLVVDENSRLVTLTCKSYLRETLATDLNKKETKLIYPPNGFISNIVE 539
DB 481 ISETFLTPINGFGLVVDENSRLVTLTCKSYLRETLATDLNKKETKLIYPPNGFISNIVE 540
QY 540 NNLFGSALKTASELJAKENLTKTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLAD 299
DB 541 NNLFGSALKTASELJAKENLTKTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLAD 300
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DB 301 IDYTSIMNEHLNKEKEEFRRVNIPLTSLNTFSNPNYKARGSDKAKIMEAKGYALVGF 360
QY 600 VKGKAALYKDEKNGDYIYEETNNLEBDFOAVTKRFTITGDSRVHLITFSONGEAFGG 659
DB 601 VKGKSIHLKDEKNGDYIYEETNNLEBDFOAVTKRFTITGDSRVHLITFSONGEAFGG 660
QY 660 NFIIEIRPSELLSPELIKSDAWYGSOGTWISGNSLINSNVNGTFRONLSLSYSTYS 719
DB 661 NFIIEIRPSELLSPELIKSDAWYGSOGTWISGNSLINSNVNGTFRONLSLSYSTYS 720
QY 720 MNFNVNGFGKVTIRNSREVVERSYLOFSSKYISEKFTTTTNNGTLYVHLSRASS--RG 776
DB 721 VYFSVSGDANVRIRNSREVLFEKRYMS-GAKDVSEMTTKPEKDNFYIELSGNNLYGCP 779
QY 777 VINFGDFSIRK 786
DB 780 IVHFYDVSIK 789

RESULT 11
Q4VYTO_BACTU
ID Q4VYTO_BACTU PRELIMINARY; PRT; 789 AA.
AC Q4VYTO;
DT 13-SEP-2005 (Tremblrel. 31, last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, last annotation update)
DB Vegetative insecticidal protein.
GN Name=vip3A;
OS Bacillus thuringiensis.

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OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RC NUCLEOTIDE SEQUENCE.  
 RP STRAIN=BTAB51;  
 RA Pham N.B., Le N.H., Pham T.T., Chu H.H., Le B.T.;  
 RT "Cloning and sequence analysis gene encoding the vegetative  
 RT insecticidal protein (VIP3a) of some Vietnamese B. thuringiensis  
 RT strains."  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ971413; CAI96522.1; -; Genomic\_DNA.  
 DR InterPro; IPR003305; Cenc Carb\_bdt.  
 DR Pfam; PF02018; CBM\_4\_9; 1.  
 KW Oxidoreductase.  
 SQ SEQUENCE 789 AA; 88614 MW; 5F255A098B9C86DD CRC64;

Query Match 79.3%; Score 3168.5; DB 2; Length 789;  
 Best Local Similarity 78.5%; Pred. No. 3.9e-140;  
 Matches 620; Conservative 70; Mismatches 95; Indels 5; Gaps 3;

QY 1 MGRN-KLSVKAALPSFIDYENGIGFATGIDIMMIFKTMGTGDLTLDLILKQOOLNE 59  
 DB 1 MNKNNTKLSRALPSFIDYENGIGFATGIDIMMIFKTDGDLTLDLILKQOOLND 60  
 QY 60 ISGLDGVNSLNDLLAQGNLDTELSEIKLKIANEQNVLDVNTKLDAINMNTYLPK 119  
 DB 61 ISGLDGVNSLNDLLAQGNLTELSEIKLKIANEQNVLDVNTKLDAINMNTYLPK 120  
 QY 120 ITSMLSVDMKNYALGQIEYLSKQLEISDKLDVINNVNLINSTEITPAYORIKYVN 179  
 DB 121 ITSMLSVDMKNYALGQIEYLSKQLEISDKLDVINNVNLINSTEITPAYORIKYVN 180  
 QY 180 EKPEALTSATETNLTQDSSHTDILDELTELAKSVTKNDVDFEFYINTPHDVMIG 239  
 DB 181 EKPEALTSATETSSKVKKDGSPADILDELTELAKSVTKNDVDFEFYINTPHDVMIG 240  
 QY 240 NNLFGRSALKTASSELIAKENLKTSGSEVGNVYNFLIVTLAQAFLLTTCRKLGLAD 299  
 DB 241 NNLFGRSALKTASSELITKENVKTSSSEVGNVYNFLIVTLAQAFLLTTCRKLGLAD 300  
 QY 300 IDYTPINMHLNKEKEEPRVNIPTLSNTFSNPYERKAGSDKDAKIIMEAKPGYALVGF 359  
 DB 301 IDYTSIMNEHLNKEKEEPRVNIPTLSNTFSNPYERKAGSDDEAKMIVEAKPGHALIGF 360  
 QY 360 EISDSIAVLKVYQAKLKHNYQIDKDSLSEIVYGDIDLCPDQSEQYITNNIVFPNEY 419  
 DB 361 EISDSITVLKVYEAKLKONYQVDDSLSEVIYGDMDKLCPDQSEQYITNNIVFPNEY 420  
 QY 420 VITKIAFTKLSLRVEVTANFYDSSGTGDIIDLNKKKISSSEAEFSMLNANNNGVYMPIGT 479  
 DB 421 VITKIDFTKMKTLRYEVTANFYDSSGTGDIIDLNKKKISSSEAEFSMLNANNNGVYMPIGT 480  
 QY 480 ISEFFLPINGFGVVDENSRLLVTLTCKSYLRETLATDLSNKKETKLIIVPNGFISNIVE 539  
 DB 481 ISEFFLPINGFGVVDENSRLLVTLTCKSYLRETLATDLSNKKETKLIIVPNGFISNIVE 540  
 QY 540 NGNLEGEMLBPMKANNKAAVYDHGCVNGTKVLYVHDEGFSQPIGDKLKTETVYIYI 599  
 DB 541 NGNLEGEMLBPMKANNKAAVYDHGCVNGTKVLYVHDEGFSQPIGDKLKTETVYIYI 600  
 QY 600 VKGKAALYLDKKNQDYIYEETNNELJDFQAVTKRFITGDSRVHLIFTSQNGEAEFGG 659  
 DB 601 VKGKPSIHLKDBENTGYIHEBDTNNLEBYQITNKRFTTGDTDLKGYVLLKLSQNGDEAMGD 660  
 QY 660 NFIISEIRPSEELLSPELIKSDAWVSGQVWISGNSLININSVNGTFPRONTSLBSYSTYS 719  
 DB 661 NFIILEISPSKELSLPELINTNNMTSTGSTWISGNTLTLVQGRGILLKQNLQDSFSTYR 720  
 QY 720 MNPNVNGGKYTINSREVPERSTLQFSSKYSISKFTTTNNNGLYVETLSRASS--RG 776  
 DB 721 VYFSVSGDANVIRNSREVLFKRYMS--GADVDSMFTTKCEKONFYELISQGNMLYGGP 779

QY 777 VINFGDSIK 786  
 DB 780 IVHFYDVSIK 789

RESULT 12  
 Q4U3F5\_BACTU  
 ID Q4U3F5\_BACTU PRELIMINARY; PRT; 789 AA.  
 AC Q4U3F5;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Vegetative insecticidal protein.  
 GN Name=VIP3A;  
 OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RC NUCLEOTIDE SEQUENCE.

RP STRAIN=LS1;

RA Lu X., Hao H., Sun S., Zhu M., Du K., Li G.;  
 RT "Vegetative insecticidal protein gene vip3A-LS1 from Bacillus  
 RT thuringiensis strain LS1."  
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; D0016968; AA041427.1; -; Genomic\_DNA.

DR InterPro; IPR003305; Cenc Carb\_bdt.

DR Pfam; PF02018; CBM\_4\_9; 1.

DR Oxidoreductase.

SQ SEQUENCE 789 AA; 88574 MW; A82803275AFEC19C CRC64;

Query Match 79.2%; Score 3163.5; DB 2; Length 789;  
 Best Local Similarity 78.4%; Pred. No. 6.7e-140;  
 Matches 619; Conservative 71; Mismatches 95; Indels 5; Gaps 3;

QY 1 MGRN-KLSVKAALPSFIDYENGIGFATGIDIMMIFKTMGTGDLTLDLILKQOOLNE 59  
 DB 1 MNKNNTKLSRALPSFIDYENGIGFATGIDIMMIFKTDGDLTLDLILKQOOLND 60  
 QY 60 ISGLDGVNSLNDLLAQGNLDTELSEIKLKIANEQNVLDVNTKLDAINMNTYLPK 119  
 DB 61 ISGLDGVNSLNDLLAQGNLTELSEIKLKIANEQNVLDVNTKLDAINMNTYLPK 120  
 QY 120 ITSMLSVDMKNYALGQIEYLSKQLEISDKLDVINNVNLINSTEITPAYORIKYVN 179  
 DB 121 ITSMLSVDMKNYALGQIEYLSKQLEISDKLDVINNVNLINSTEITPAYORIKYVN 180  
 QY 180 EKPEALTSATETNLTQDSSHTDILDELTELAKSVTKNDVDFEFYINTPHDVMIG 239  
 DB 181 EKPEALTSATETSSKVKKDGSPADILDELTELAKSVTKNDVDFEFYINTPHDVMIG 240  
 QY 240 NNLFGRSALKTASSELIAKENLKTSGSEVGNVYNFLIVTLAQAFLLTTCRKLGLAD 299  
 DB 241 NNLFGRSALKTASSELITKENVKTSSSEVGNVYNFLIVTLAQAFLLTTCRKLGLAD 300  
 QY 300 IDYTPINMHLNKEKEEPRVNIPTLSNTFSNPYERKAGSDKDAKIIMEAKPGYALVGF 359  
 DB 301 IDYTSIMNEHLNKEKEEPRVNIPTLSNTFSNPYERKAGSDDEAKMIVEAKPGHALIGF 360  
 QY 360 EISDSIAVLKVYQAKLKHNYQIDKDSLSEIVYGDIDLCPDQSEQYITNNIVFPNEY 419  
 DB 361 EISDSITVLKVYEAKLKONYQVDDSLSEVIYGDMDKLCPDQSEQYITNNIVFPNEY 420  
 QY 420 VITKIAFTKLSLRVEVTANFYDSSGTGDIIDLNKKKISSSEAEFSMLNANNNGVYMPIGT 479  
 DB 421 VITKIDFTKMKTLRYEVTANFYDSSGTGDIIDLNKKKISSSEAEFSMLNANNNGVYMPIGT 480  
 QY 480 ISEFFLPINGFGVVDENSRLLVTLTCKSYLRETLATDLSNKKETKLIIVPNGFISNIVE 539  
 DB 481 ISEFFLPINGFGVVDENSRLLVTLTCKSHRELLATDLSNKKETKLIIVPNGFISNIVE 540  
 QY 540 NGNLEGEMLBPMKANNKAAVYDHGCVNGTKVLYVHDEGFSQPIGDKLKTETVYIYI 599  
 DB 541 NGNLEGEMLBPMKANNKAAVYDHGCVNGTKVLYVHDEGFSQPIGDKLKTETVYIYI 600

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Db 541 NSGIEEDNLEPWKANKNAAYDHTGCVNGTKALYYHKDGGISQFIGDKLKPKTEVYIOYT 600
QY 600 VKGKAAIYLDKDKNGDYIYEETNNLEDFQAVTKRFTIGTDSRVHLFTSONGGEARFG 659
Db 601 VKGKASIFLKDKNENYIYEDTNNLEEDYQITNKFTTGTDLKGVLLIKSQNGDEAWGD 660
QY 660 NFIISEIRPSEBELLSPELIKSDAWVGSQGTWISGNSLINSNVNGTFRQNTLSBSYSTYS 719
Db 661 NFIILEISPCCKLSPBLIKTDKMNSTGSTYISDRRLTYRGGRGILKQNLQDGFSTYR 720
QY 720 MNFNNGRGKXTIRNSREVVERSTYLOPSSKXISEKFTTTNNGLYVELSRASG--RG 776
Db 721 VYFSVSGDANVIRINSREVLLEKRYLS-GAKOVSEMFYTKFKDKNFYIELSQGNMLYGGP 779
QY 777 VINFQDPSIK 786
Db 780 IYHFYDSIK 789

RESULT 13
Q5JZY9_BACTU PRELIMINARY; PRT; 786 AA.
ID Q5JZY9_BACTU PRELIMINARY; PRT; 786 AA.
AC Q5JZY9_
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Isp3b protein.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Van Rie J., Arnaut G., Boers A., Damme N.;
RT "Genes encoding insecticidal secreted proteins from Bacillus
thuringiensis.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ872071; CAI43276.1; -; Genomic DNA.
DR GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005975; F:carbohydrate metabolism; IEA.
DR InterPro; IPR003305; CEM_CenC.
DR Pfam; PF02018; CEM_4_9; 1.
KM Oxidoreductase.
SQ SEQUENCE 786 AA; 88997 MW; B67FD67CBA56A57 CRC64;

Query Match 79.1%; Score 3160; DB 2; Length 786;
Best Local Similarity 78.6%; Pred. No. 9, 7e-140;
Matches 619; Conservative 74; Mismatches 91; Indels 4; Gaps 3;

QY 1 MQKNN-KLSVKALPSFIDYFNGIGYGFATGIDKIDNMIRKNTGSLTDELILKNOQLNE 59
Db 1 MNMNNAKIMARLPSFIDYFNGIGYGFATGIDKIDNMIRKNTGSLTDELILKNOQLNE 60
QY 60 ISGKLDGVNGSLNDLLAQGNLDTLSKEILKIANEONKVNDVNTKDAINMLMTYLPK 119
Db 61 ISGKLDGVNGSLNDLLAQGNLDTLSKEILKIANEONKVNDVNTKDAINMLMTYLPK 120
QY 120 ITSMUSDVMKQNYALGQIEYLSKQKEISDRLDVINNVNLINSTLTETPAYQRICKYV 179
Db 121 ITSMUSDVMKQNYVLSQIEYLSKQKEISDRLDVINNVNLINSTLTETPAYQRICKYV 180
QY 180 EKPELTSATETNLTKTQDSSHTDILDELTELAKSVTKNDVDGFEFYANTFHDVWG 239
Db 181 EKPELTSATETNLTKTQDSSHTDILDELTELAKSVTKNDVDGFEFYANTFHDVWG 240
QY 240 NNLFGRSALKTASSELIAKENLKTSGSEYGVNYPFLIVTALQAKAFLTLTCKRLGLAD 299
Db 241 NNLFGRSALKTASSELIAKENLKTSGSEYGVNYPFLIVTALQAKAFLTLTCKRLGLAD 300
QY 300 IDYPIPMNEHLNKEKEEFRRVNLPLTSLNTFSNPYEKARGSDKAKIIMEAKPGYALVF 359
Db 301 IDYPIPMNEHLNKEKEEFRRVNLPLTSLNTFSNPYEKARGSDKAKIIMEAKPGYALVF 360

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QY 360 BISXDSIAVLKYKYOAKLKHNVQIDKDSLSSEIYVGDIDKLCPDQSEOMYTTKIAFPNEY 419
Db 361 EMSNDSTIYVLKAYQMLKKDVOIDKDSLSSEIYVGDIDKLCPDQSEOMYTTKIAFPNEY 420
QY 420 VITKIAFTKQNLSEYEVYANFYDSSTGIDILNKKKISSSEAFSEMLNANDGVMPICG 479
Db 421 VITKIAFTKQNLSEYEVYANFYDSSTGIDILNKKKISSSEAFSEMLNANDGVMPICG 480
QY 480 ISETFLTPINGFLVYDENSRLVLTCKSYARETLATDLSKETEKLIVPENGFISSNIVE 539
Db 481 ISETFLTPINGFLVYDENSRLVLTCKSYARETLATDLSKETEKLIVPENGFISSNIVE 540
QY 540 NGNLEGENLEPWKANKNAAYDHTGCVNGTKLYHHEGSESOFIGDKLKPKTEVYIOYT 599
Db 541 NGNLEMDTLEPWKANKNAAYDHTGCVNGTKLYHHEGSESHFIGDKLKPKTEVYIOYT 600
QY 600 VKGKAAIYLDKDKNGDYIYEETNNLEDFQAVTKRFTIGTDSRVHLFTSONGGEARFG 659
Db 601 VKGKASIFLKDKNENYIYEDTNNLEEDYQITNKFTTGTDLKGVLLIKSQNGDEAWGD 660
QY 660 NFIISEIRPSEBELLSPELIKSDAWVGSQGTWISGNSLINSNVNGTFRQNTLSBSYSTYS 719
Db 661 NFIILEISPCCKLSPBLIKTDKMNSTGSTYISDRRLTYRGGRGILKQNLQDGFSTYR 720
QY 720 MNFNNGRGKXTIRNSREVVERSTYLOPSSKXISEKFTTTNNGLYVELSRASRG-VI 778
Db 721 VYFSVSGDANVIRINSREVLLEKRYL--NRGVSSEMFYTKFKDNFYVELSQGNMLGTV 778
QY 779 NFGDPSIK 786
Db 779 HFYDPSIK 786

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RESULT 14
Q4U3F4_BACTU PRELIMINARY; PRT; 789 AA.
ID Q4U3F4_BACTU PRELIMINARY; PRT; 789 AA.
AC Q4U3F4_
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Vegetative insecticidal protein.
GN Name=vip3A;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lu X., Hao H., Sun S., Zhu M., Du K., Li G.;
RT "Vegetative insecticidal protein gene vip3A-Ls8 from Bacillus
thuringiensis strain LS8.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; DQ016969; AA41428.1; -; Genomic DNA.
DR InterPro; IPR003305; CEM_cenC-bd.
DR Pfam; PF02018; CEM_4_9; 1.
KM Oxidoreductase.
SQ SEQUENCE 789 AA; 88540 MW; D4A09EDA53898B3 CRC64;

Query Match 79.1%; Score 3159.5; DB 2; Length 789;
Best Local Similarity 78.2%; Pred. No. 1e-139;
Matches 618; Conservative 70; Mismatches 97; Indels 5; Gaps 3;

QY 1 MQKNN-KLSVKALPSFIDYFNGIGYGFATGIDKIDNMIRKNTGSLTDELILKNOQLNE 59
Db 1 MNMNNAKIMARLPSFIDYFNGIGYGFATGIDKIDNMIRKNTGSLTDELILKNOQLNE 60
QY 60 ISGKLDGVNGSLNDLLAQGNLDTLSKEILKIANEONKVNDVNTKDAINMLMTYLPK 119
Db 61 ISGKLDGVNGSLNDLLAQGNLDTLSKEILKIANEONKVNDVNTKDAINMLMTYLPK 120
QY 120 ITSMUSDVMKQNYALGQIEYLSKQKEISDRLDVINNVNLINSTLTETPAYQRICKYV 179

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Db	121	ITSLMSDWMKQNYATSLQLEIYSKQQLSEIDSKDIIINAVNLNSTLITETTPAYQRIKYV	180
Qy	180	EKFEALTATETNTLKTQDSSHTDILDELTELTELAKSVTKNDVDGFEFYNTFHDVMIG	239
Db	181	EKFEELATATETTSKVKKDGSPADILDELTELTELAKSVTKNDVDGFEFYNTFHDVMIG	240
Qy	240	NNLFGRSALKTASBELITKENVKTSGSGVGNVNFILVLTALQAKAFLLTTCKRLGLAD	299
Db	241	NNLFGRSALKTASBELITKENVKTSGSGVGNVNFILVLTALQAKAFLLTTCKRLGLAD	300
Qy	300	IDYDPIMNEHINKEKEEPRVNLPTLSNFSNPNEKAGSKDAKIMEARPGVALNP	359
Db	301	IDYTSIMNEHINKEKEEPRVNLPTLSNFSNPNAKVGSBDAAMIVEARGHALIG	360
Qy	360	EISKDSIAVLKYOQAKLKHNYOIDDLSLSEIYVGDIDKLCPDQSEOMYYTNKIAFPNEX	419
Db	361	EISNDSTIVLKYTEAKLKNQYVDKDSLSEVLYGMDKLLCPDQSEQIYTTNNIYFPNEX	420
Qy	420	VITKIAFTFKLNSLREYVATANFYDSSGTGDIINKKKISSSEAFSMANANDGVMPIGT	479
Db	421	VITKIDPFTKKMKTLLREYVATANFYDSSGTGEIDLNKKKVESSSEAYRTLSSANDGVMPIGV	480
Qy	480	ISEFTPLTINGGLVVDENSRLLVTLTCKSVTAETLLATPLSKETGLIYPPNFIINYE	539
Db	481	ISEFTPLTINGGLQADENSRLLITLTCKSVTLRELLATPLSKETGLIYPPSPGISNIYE	540
Qy	540	NGNLGEMNLPEPKANNKAYVDHTGSGVNTKYLVIYARDEFSQIFIDKLLKTEYVIOYI	599
Db	541	NGSIEDNLEPEPKANNKAYVDHTGSGVNTKALVYHKDGGISQIFIDKLLKPTREYVIOYT	600
Qy	600	VKGKAIYLYDKERKNDYIYEETNNLEDFQAVTKRPIGTGDSRSHLIFTSONGEEAFGG	659
Db	601	VKGKPSIHLKDENTGYIHVEDTNNNLEDYQITNKRPFTGTDLKGVYLLILKSQNGDEAMGD	660
Qy	660	NFIISEIRPSEBLLSPELILKSADWVGSOGTWSGNSLNNSVNGTFPRQNLSEISTYS	719
Db	661	NFIILIEIPSEBLLSPELINTNNMTSTGTSINTSGNTLLTYOGGRGLIKQNLQDPSFYR	720
Qy	720	MNFNVNGGKWTIRNSREYVPEFSRYLQFSSKTISEKFTTNNNTGILYVELSRSS--RG	776
Db	721	VYFSVSGDANVATIRNSREYVLEFKRYS-CAKOVSEKFTTKFEKDNFYIELSQANNLYGCP	779
Qy	777	VINFGDFPSIK 786	
Db	780	IYHFYDVSIX 789	
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AC	Q45793_		
DT	01-NOV-1996	(TREMBLrel. 01, Created)	
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)	
DE	Insecticidal protein.		
GN	Name=Viip3A(b);		
OS	Bacillus thuringiensis.		
OC	Bacteria, Firmicutes, Bacillales; Bacillaceae; Bacillus;		
OC	Bacillus cereus group.		
OX	NCBI_TaxID=1428;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=AB424;		
RX	MEDLINE=96224295; PubMed=8643585; DOI=10.1073/pnas.93.11.5389;		
RA	Estuch J.J., Warren G.W., Mullins M.A., Nye G.J., Craig J.A.,		
RA	Kozielec M.G.;		
RT	"Viip3A", a novel Bacillus thuringiensis vegetative insecticidal protein		
RT	with a wide spectrum of activities against lepidopteran insects.",		
RL	Proc. Natl. Acad. Sci. U.S.A. 93:5389-5394(1996).		
DR	EMBL, L48812; AACJ7037.1; - Genomic DNA.		
DR	GO; GO:0016491; P:oxidoreductase activity; IEA.		
DR	InterPro; IPR003305; CBM Cenc.		

DR Pfam: PF02019; CBM\_4\_9; 1.  
SQ OxiReductase.  
KM SEQUENCE 789 AA; 88638 MW; 754969B452C54138 CRC64;  
Query Match 79.0%; Score 3156.5; DB 2; Length 789;  
Best Local Similarity 78.2%; Pred. No. 1,4e-139;  
Matches 618; Conservative 70; Mismatches 97; Indels 5; Gaps 3.

QY 1 MOKNN-KLSVRLPSFIDYFNGIYGFATGIDKIDINMIFKTNFGDGLTDELKNOQLINE 59  
DB 1 MNKNNTKLTSTALSPSIFIDYFNGIYGFATGIDKIDINMIFKTDGTDELDELKNOQLIND 60  
QY 60 ISGLDVGNSLNDLLAQGNLDTELSEKILKIANQKQVNDVMTKDAINLMTVLPK 119  
DB 61 ISGKLDVGNSLNDLLAQGNLNTLSKILKIANQKQVNDVNNKLDALNTMLRVLPK 120  
QY 120 ITSMUSDVKNQVNLGLQIEYLSKOLKEISPKLDVINNVNLINSTLTETPAYQRIKYVN 179  
DB 121 ITSMUSDVKNQVNLGLQIEYLSKOLKEISPKLDVINNVNLINSTLTETPAYQRIKYVN 180  
QY 180 EKFEALTSATETNLKTKQDSSHITLDELTELTELIAKSVTKNDVDGFEFYLTFFDVMIG 239  
DB 181 EKFEELTPATESTSKVKKDGSPADIRDELTELTELAKSVTKNDVDGFEFYLTFFDVMVG 240  
QY 240 NNLPERSALKTPASELIAKEMLKTGGSFVGNGVYNNFLIVTALQAKAFLLTPCRKLLGLAD 299  
DB 241 NNLPERSALKTPASELITKENVKTGSSEVGANYNPLIVTALQAKAFLLTPCRKLLGLAD 300  
QY 300 IDYTPINNEHLENKEKEEPRVANILPTLSVTFSPNPKYERKAGSDKDAKIMAEKPGYALVGF 359  
DB 301 IDYTSINNEHLENKEKEEPRVANILPTLSVTFSPNPKYAKYKGSDEDAKMIVEAKPGHALIGF 360  
QY 360 EISKDSIALVLKVYQAKLKHNYQIDKDSISELIVGDIDLKCPDQSEQMYTNKIAFENNEY 419  
DB 361 EISNDSITVLKVEYEAKLKQNYQVDPKDSLEVIYGDMDKLLCPDQSGQIYTNINNIYFENEY 420  
QY 420 VITKLAFLPKKALNSLRLEYTANFYDSSSTDIDLANKKKEISSAEPSFSLMANNDGVYMPGCT 479  
DB 421 VITKIDFLPKKOKTLEYEYATNFYDSSSTEBIDLANKKKESSAEKFRITLISANDGVYMPGIV 480  
QY 480 ISETPLTPINGFGLVVDNSRLVLTLTCKSYARETLTADLSENKETKLIVPPNGFSINIVE 539  
DB 481 ISETPLTPINGFGLQADENSRLITLTCKSYARELLIADLSENKETKLIVPPSPGISNIVE 540  
QY 540 NGNLEGENILBPMKANNNKNAAYVDHTGGVNGTIVLVYHEDGEFSQFIGDKLKTETEVIOYI 599  
DB 541 NGSIEEDNLBPMKANNNKNAAYVDHTGGVNGTIVLVYHKGQGSQFIGDKLKTETEVIOYT 600  
QY 600 VKGKRAILYKDBKNGDIYIESTNNLELPQAVTKRFITGTSSSRPHLLFTSQNGEAEAGG 659  
DB 601 VKGKPSIHLKDBNGDIYIHYEDTNNLLEBYQITINRFTTGTDLKGYYLLILKQNGGEAAGD 660  
QY 660 NFIISEIRPSEELSPELIKSDAWGSGQVWISGNSLINSNVNGTFRONLSLESYSTYS 719  
DB 661 NFIIIEISPSEKTLSPELINTNNMTSTGTSITLTYGQGRGILKQNLQDBSFSTYR 720  
QY 720 MNFNVNGGKTYIIRNSREVEVERSTYLOPSKXYISEKFTTTNNMTGLYYELBRASS--RG 776  
DB 721 VYFSVSGDANVRIRNSREVLFEKRYMS-GADVDSMFTTFKEKONFYIELSGNNLYGGP 779  
QY 777 VINFGDPSIK 786  
DB 780 IVHFPYDVSIK 789



GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 15, 2006, 20:43:31 ; Search time 47 Seconds  
(without alignments)  
1382.619 Million cell updates/sec

Title: US-10-698-096-17

Perfect score: 3395  
Sequence: 1 MQKNKLKSVKALPSFIDYFN.....VELSRASSRGVINFDFSIK 786

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2\_6/ptodata/1/1aa/H COMB.pep.\*  
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5: /cgn2\_6/ptodata/1/1aa/RE COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3505	87.7	787	2	US-09-307-106-54 Sequence 54, Appl
2	3182.5	79.7	789	2	US-09-002-285-82 Sequence 82, Appl
3	3182.5	79.7	789	2	US-09-589-477-82 Sequence 82, Appl
4	3182.5	79.7	789	2	US-10-099-285A-82 Sequence 82, Appl
5	3180.5	79.6	789	2	US-09-002-285-84 Sequence 84, Appl
6	3180.5	79.6	789	2	US-09-589-477-84 Sequence 84, Appl
7	3180.5	79.6	789	2	US-10-099-285A-84 Sequence 84, Appl
8	3176.5	79.5	789	2	US-09-002-285-92 Sequence 92, Appl
9	3176.5	79.5	789	2	US-09-589-477-92 Sequence 92, Appl
10	3176.5	79.5	789	2	US-10-099-285A-92 Sequence 92, Appl
11	3175.5	79.5	790	2	US-08-960-780-8 Sequence 8, Appl
12	3175.5	79.5	790	2	US-09-073-898-8 Sequence 8, Appl
13	3175.5	79.5	790	2	US-09-307-106-2 Sequence 2, Appl
14	3175.5	79.5	789	2	US-09-850-351A-8 Sequence 8, Appl
15	3171.5	79.4	789	2	US-08-471-033-29 Sequence 29, Appl
16	3171.5	79.4	789	1	US-08-471-044-29 Sequence 29, Appl
17	3171.5	79.4	789	1	US-08-463-483A-29 Sequence 29, Appl
18	3171.5	79.4	789	1	US-08-471-046A-29 Sequence 29, Appl
19	3171.5	79.4	789	1	US-08-470-566B-29 Sequence 29, Appl
20	3171.5	79.4	789	1	US-08-838-219B-2 Sequence 2, Appl
21	3171.5	79.4	789	1	US-08-469-334-29 Sequence 29, Appl
22	3171.5	79.4	789	2	US-09-300-529-29 Sequence 29, Appl
23	3171.5	79.4	789	2	US-09-233-336A-2 Sequence 2, Appl
24	3171.5	79.4	789	2	US-09-233-752A-2 Sequence 2, Appl
25	3171.5	79.4	789	2	US-09-402-036-2 Sequence 2, Appl
26	3171.5	79.4	789	2	US-09-904-226-2 Sequence 2, Appl
27	3170.5	79.4	789	2	US-09-002-285-78 Sequence 78, Appl

28	3170.5	79.4	789	2	US-09-002-285-94 Sequence 94, Appl
29	3170.5	79.4	789	2	US-09-002-285-96 Sequence 96, Appl
30	3170.5	79.4	789	2	US-09-589-477-78 Sequence 78, Appl
31	3170.5	79.4	789	2	US-09-589-477-94 Sequence 94, Appl
32	3170.5	79.4	789	2	US-09-589-477-96 Sequence 96, Appl
33	3170.5	79.4	789	2	US-10-099-285A-78 Sequence 78, Appl
34	3170.5	79.4	789	2	US-10-099-285A-94 Sequence 94, Appl
35	3170.5	79.4	789	2	US-10-099-285A-96 Sequence 96, Appl
36	3167.5	79.3	789	2	US-08-960-780-6 Sequence 6, Appl
37	3167.5	79.3	789	2	US-09-073-898-6 Sequence 6, Appl
38	3167.5	79.3	789	2	US-09-850-351A-6 Sequence 6, Appl
39	3158.5	79.1	790	2	US-08-960-780-4 Sequence 4, Appl
40	3158.5	79.1	790	2	US-09-073-898-4 Sequence 4, Appl
41	3158.5	79.1	790	2	US-09-850-351A-4 Sequence 4, Appl
42	3156.5	79.0	789	1	US-08-471-033-32 Sequence 32, Appl
43	3156.5	79.0	789	1	US-08-471-044-32 Sequence 32, Appl
44	3156.5	79.0	789	1	US-08-463-483A-32 Sequence 32, Appl
45	3156.5	79.0	789	1	US-08-471-046A-32 Sequence 32, Appl

#### ALIGNMENTS

RESULT 1  
US-09-307-106-54  
Sequence 54, Application US/09307106  
Patent No. 6603063  
GENERAL INFORMATION:  
APPLICANT: Fetteleson, Jerald S.  
APPLICANT: Schepf, H. Ernest  
APPLICANT: Narva, Kenneth B.  
APPLICANT: Stockhoff, Brian A.  
APPLICANT: Schneits, James  
APPLICANT: Loewer, David  
APPLICANT: Dullum, Charles Joseph  
APPLICANT: Muller-Cohn, Judy  
APPLICANT: Stamp, Lisa  
APPLICANT: Morrill, George  
APPLICANT: Fintad-Lee, Stacey  
TITLE OF INVENTION: No. 6603063el Pesticidal Toxins and Nucleotide  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/307,106  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/960,780  
FILING DATE: 30-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/073,898  
FILING DATE: 05-MAY-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-708C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100

TELEFAX: 352-372-5800  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 787 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-307-106-54

Query Match 87.7%; Score 3505; DB 2; Length 787;  
Best Local Similarity 87.1%; Pred. No. 1.5e-239;

Matches 682; Conservative 45; Mismatches 56; Indels 0; Gaps 0;

QY 4 NKKLSVAKLPSPFDYFNGIYGFATGIKDIMMIFKNTGGLTDEILKNQQLNEISGK 63  
DB 5 NTKLMNAPLPSFDYFNGIYGFATGIKDIMMIFKNTGGLTDEILKNQQLNEISGK 64  
QY 64 LDGNGSLNDLLAOGNLTDELTELAKSVTKNDVDGFEFYLTFFHDMVIG 123  
DB 65 LDGNGSLNDLLAOGNLTDELTELAKSVTKNDVDGFEFYLTFFHDMVIG 124  
QY 124 LSDVMKQNYALGLQIEYLSKQLEISDKLDVINNVVLINSTLTETPAVQRIKYNKEPE 183  
DB 125 LSDVMKQNYALSLQVEYLSKQLEISDKLDVINNVVLINSTLTETPAVQRIKYNKEPE 184  
QY 184 ALTSATEINLKTKDSSHTDILDELTELTELAKSVTKNDVDGFEFYLTFFHDMVIG 243  
DB 185 ELTFATETTLTKVKKQDSSPADILDELTELTELAKSVTKNDVDGFEFYLTFFHDMVIG 244  
QY 244 GRSALKTKASELIAKENLKTSGSEGVGNVNFILVLTALQAKAFLTLTTCRKILGLAD 303  
DB 245 GRSALKTKASELIAKENLKTSGSEGVGNVNFILVLTALQAKAFLTLTTCRKILGLAD 304  
QY 304 PINNEHLNKEKEPERVNIPLTSLNTFSPNPEYKARGSDKAKIMEAKPGVALVGEISK 363  
DB 305 SINNEHLNKEKEPERVNIPLTSLNTFSPNPEYKARGSDKAKIMEAKPGVALVGEISK 364  
QY 364 DSIAVLKLYQAKLKHNYQIDKDSLSEIVYGDIDQLCPDSEQWYTNKLAFPNEVYITK 423  
DB 365 DSMTVLKYBAKCKONQVDDKSLSEVYISYDMDKLCPDSEQWYTNKLAFPNEVYITK 424  
QY 424 IAPTKLNSLRFEYTNANFYSSTGDDIDLANKKILSSSAEFSMLNANDGVYMPIGTSET 483  
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DB 605 AATLYLDERKGDYIYETTNNELEDPAVYTRFITGDDSSVYHLIFTSQNGEBAPGAFI 664  
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DB 665 SEIRPSELISPELISDAWVSGQTMISGNSLINSNVNGTFRONLPLESYSTYSNFT 724  
QY 724 VNGFGKVTJNSREVVERSYLOFSKYLSEKFTYTTNNTGLVVELSRASSRGVINGDF 783  
DB 725 VNGFGKVTJNSREVVERSYLOFSKYLSEKFTYTTNNTGLVVELSRASSRGVINGDF 784  
QY 784 SIR 786  
DB 785 SIR 787

RESULT 2  
US-09-002-285-82

Sequence 82, Application US/09002285  
Patent No. 6369213  
GENERAL INFORMATION:  
APPLICANT: Schepf, H. Ernest  
APPLICANT: Wicker, Carol  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Walz, Michelle  
APPLICANT: Stockhoff, Brian  
APPLICANT: Muller-Cohn, Judy  
TITLE OF INVENTION: Toxins Active Against Pests  
NUMBER OF SEQUENCES: 105  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/002,285  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/886,615  
FILING DATE: 1-JUL-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/674,002  
FILING DATE: 1-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-701C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-002-285-82

Query Match 79.7%; Score 3182.5; DB 2; Length 789;  
Best Local Similarity 79.0%; Pred. No. 9.9e-217;

Matches 624; Conservative 69; Mismatches 92; Indels 5; Gaps 3;

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QY 60 ISGKLDGNGSLNDLLAOGNLTDELTELAKSVTKNDVDGFEFYLTFFHDMVIG 119  
DB 61 ISGKLDGNGSLNDLLAOGNLTDELTELAKSVTKNDVDGFEFYLTFFHDMVIG 120  
QY 120 ITSMUSDVMKQNYALGLQIEYLSKQLEISDKLDVINNVVLINSTLTETPAVQRIKYN 179  
DB 121 ITSMUSDVMKQNYALSLQVEYLSKQLEISDKLDVINNVVLINSTLTETPAVQRIKYN 180  
QY 180 EKFEALTSATEINLKTKDSSHTDILDELTELTELAKSVTKNDVDGFEFYLTFFHDMVIG 239  
DB 181 EKFEALTSATEINLKTKDSSHTDILDELTELTELAKSVTKNDVDGFEFYLTFFHDMVIG 240  
QY 240 NNLFGRSALKTKASELIAKENLKTSGSEGVGNVNFILVLTALQAKAFLTLTTCRKILGLAD 299  
DB 241 NNLFGRSALKTKASELIAKENLKTSGSEGVGNVNFILVLTALQAKAFLTLTTCRKILGLAD 300

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Qy 300 IDYTPINNEHLNKEKEEFVRNIIPTLSNTFSPNPKYKARSGDKAKIIMEAKPGYALVGF 359
Db 301 IDYTSINNEHLNKEKEEFVRNIIPTLSNTFSPNPKYKARSGDEBKAKIIMEAKPGYALVGF 360
Qy 360 EISKDSIAVLKTYQAKLKHNTQIDKDSLSSEIYVGDIDKLCPODSEQMYTNNKIAFPNEY 419
Db 361 EMSNDSITVLKYVEAKLKQNYQVDDKSLSEVYIGDTDLCPDQSEQIYYTNNIYVFPNEY 420
Qy 420 VITKIAPTKLNSLRVEVTANFYDSSGTGDIIDKKKIESSEAEBSMANNNDGYMPTIGT 479
Db 421 VITKIDTKKOKTLRHEVTANFYDSSGTGDIIDKKKIESSEAEBSMANNNDGYMPTIGV 480
Qy 480 ISETFLTPINGFGLVVDENSRLLVTLCKSYLRETLATDLSNKEKTLVPPNGFISNIVE 539
Db 481 ISETFLTPINGFGLVVDENSRLLVTLCKSYLRETLATDLSNKEKTLVPPNGFISNIVE 540
Qy 540 NGNLEGERLEPWKANNKNAAYDHTGCVNGTYLVYHEDGEFSQFIGDKLKTEVYIQT 599
Db 541 NGNLEGERLEPWKANNKNAAYDHTGCVNGTYLVYHEDGEFSQFIGDKLKTEVYIQT 600
Qy 600 VKGAATYIKDEKNGDIYEETNNELDPOAVTKRFTIGTDSRVHLIFTSONGEBAAG 659
Db 601 VKGAPSIHLKDEKNGTYIHEBDTNNLKDYQITTKRFTTGTDLKGVYLLKSGNGDEAWGD 660
Qy 660 NFIISEIRPSEELLSPBLIKSDAWVSGQTWISGNSLINSNVNGTFRONTLSSESTYS 719
Db 661 NFIISEIRPSEELLSPBLIKSDAWVSGQTWISGNSLINSNVNGTFRONTLSSESTYS 720
Qy 720 MNRVNGRGKVTIRNSREVFERSYLOFSKYSIKFTTTTNTGLVYELSRASS--RG 776
Db 721 VYFVSQSGANVRIRNSREVLFEKRYMS-GAKDVSEMFTEKFEKONFYIELSQNNLYGCP 779
Qy 777 VINFGDPSIK 786
Db 780 IVHFNDSIK 789

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RESULT 3  
US-09-589-477-82  
Sequence 82, Application US/09589477

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: Patent No. 6570005
: GENERAL INFORMATION:
: APPLICANT: Schepf, H. Ernest
: APPLICANT: Wicker, Carol
: APPLICANT: Narva, Kenneth E.
: APPLICANT: Walz, Michelle
: APPLICANT: Stockhoff, Brian
: TITLE OF INVENTION: Toxins Active Against Pests
: NUMBER OF SEQUENCES: 105
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: Florida
: COUNTRY: USA
: ZIP: 32606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/589,477
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/886,615
: FILING DATE: 1-JUL-1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/674,002
: FILING DATE: 1-JUL-1996
: CLASSIFICATION:

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: ATTORNEY/AGENT INFORMATION:
: NAME: Sanders, Jay M. 39,355
: REGISTRATION NUMBER: 39,355
: REFERENCE/DOCKET NUMBER: NA-701C1C1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (352) 375-8100
: TELEFAX: (352) 372-5800
: INFORMATION FOR SEQ ID NO: 82:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 789 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-589-477-82
Query Match 79.7%; Score 3182.5; DB 2; Length 789;
Best Local Similarity 79.0%; Pred. No. 9.9e-217;
Matches 624; Conservative 69; Mismatches 92; Indels 5; Gaps 3;
Qy 1 MOKN-KLSYKALPSPIDYRNGIYGFATGKIDIMMIFKTNNGDILDEILKQOOLINE 59
Db 1 MNKNNTKLSRALPSFIDYFNGIYGFATGKIDIMMIFKTDYGGNLTLDLILKQOOLINE 60
Qy 60 ISGLDGVNGSLNDLQGNLDPELSKEILKIANEOKVLDVNTKLDATIMAMNTYLPK 119
Db 61 ISGLDGVNGSLNDLQGNLNTLSKEILKIANEQVQVNDVNNKLDATIMAMNTYLPK 120
Qy 120 ITSMLSVDMQNVYALGLQIEYLSKOLKEISDKLDVINVNLINSTLEITPAYORIKYVN 179
Db 121 ITSMLSVDMQNVYALGLQIEYLSKOLKEISDKLDVINVNLINSTLEITPAYORIKYVN 180
Qy 180 EKFEALTSAETNLIKTKQDSSHTDILDELTBELFLAKSVTKNDVGEFFYLNTHFDMVG 239
Db 181 EKFEALTSAETNLIKTKQDSSHTDILDELTBELFLAKSVTKNDVGEFFYLNTHFDMVG 240
Qy 240 NNLFGRSALKTASSELAKENLKTSGSEVGNVNFYLVTLQAKAFLLTTCRRLGLAD 299
Db 241 NNLFGRSALKTASSELAKENLKTSGSEVGNVNFYLVTLQAKAFLLTTCRRLGLAD 300
Qy 300 IDYTPINNEHLNKEKEEFVRNIIPTLSNTFSPNPKYKARSGDKAKIIMEAKPGYALVGF 359
Db 301 IDYTSINNEHLNKEKEEFVRNIIPTLSNTFSPNPKYKARSGDEBKAKIIMEAKPGYALVGF 360
Qy 360 EISKDSIAVLKTYQAKLKHNTQIDKDSLSSEIYVGDIDKLCPODSEQMYTNNKIAFPNEY 419
Db 361 EMSNDSITVLKYVEAKLKQNYQVDDKSLSEVYIGDTDLCPDQSEQIYYTNNIYVFPNEY 420
Qy 420 VITKIAPTKLNSLRVEVTANFYDSSGTGDIIDKKKIESSEAEBSMANNNDGYMPTIGT 479
Db 421 VITKIDTKKOKTLRHEVTANFYDSSGTGDIIDKKKIESSEAEBSMANNNDGYMPTIGV 480
Qy 480 ISETFLTPINGFGLVVDENSRLLVTLCKSYLRETLATDLSNKEKTLVPPNGFISNIVE 539
Db 481 ISETFLTPINGFGLVVDENSRLLVTLCKSYLRETLATDLSNKEKTLVPPNGFISNIVE 540
Qy 540 NGNLEGERLEPWKANNKNAAYDHTGCVNGTYLVYHEDGEFSQFIGDKLKTEVYIQT 599
Db 541 NGNLEGERLEPWKANNKNAAYDHTGCVNGTYLVYHEDGEFSQFIGDKLKTEVYIQT 600
Qy 600 VKGAATYIKDEKNGDIYEETNNELDPOAVTKRFTIGTDSRVHLIFTSONGEBAAG 659
Db 601 VKGAPSIHLKDEKNGTYIHEBDTNNLKDYQITTKRFTTGTDLKGVYLLKSGNGDEAWGD 660
Qy 660 NFIISEIRPSEELLSPBLIKSDAWVSGQTWISGNSLINSNVNGTFRONTLSSESTYS 719
Db 661 NFIISEIRPSEELLSPBLIKSDAWVSGQTWISGNSLINSNVNGTFRONTLSSESTYS 720
Qy 720 MNRVNGRGKVTIRNSREVFERSYLOFSKYSIKFTTTTNTGLVYELSRASS--RG 776
Db 721 VYFVSQSGANVRIRNSREVLFEKRYMS-GAKDVSEMFTEKFEKONFYIELSQNNLYGCP 779
Qy 777 VINFGDPSIK 786

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CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/886,615  
FILING DATE: 1-JUL-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/674,002  
FILING DATE: 1-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-701C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-002-285-84

Query Match 79.6%; Score 3180.5; DB 2; Length 789;  
Best Local Similarity 78.9%; Pred. No. 1.4e-216;  
Matches 623; Conservative 70; Mismatches 92; Indels 5; Gaps 3;

QY 1 MOKNN-KLSYKALPSFIDYNGIYGPATGIDIMNMIFKNTMGDLTDLILKNOQLNE 59  
DB 1 MNNKNTKLSARALPSFIDYNGIYGPATGIDIMNMIFKNTMGDLTDLILKNOQLNE 60  
QY 60 ISGRLDGVNGSLNDLAAQGNLDTELSKEILKIANEONKVLNDVNTKLDAINMLNTYLPK 119  
DB 61 ISGRLDGVNGSLNDLAAQGNLDTELSKEILKIANEONKVLNDVNTKLDAINMLNTYLPK 120  
QY 120 ITSMLSDMKONVYALGLQIEYLSKQLEISPKLDVINNVLIINSTLEITPAYORIKYVN 179  
DB 121 ITSMLSDMKONVYALGLQIEYLSKQLEISPKLDVINNVLIINSTLEITPAYORIKYVN 180  
QY 180 EKFEALTSATETNKTODSSHTDILDELTELSAASVTNDVDGPEFYANTHVDWIG 239  
DB 181 EKFEALTSATETNKTODSSHTDILDELTELSAASVTNDVDGPEFYANTHVDWIG 240  
QY 240 NNLFGRSALKTASELIAKENIKTSSEYGVNYPFLIVLTALQAKAFLLTTCRKLGLAD 299  
DB 241 NNLFGRSALKTASELIAKENIKTSSEYGVNYPFLIVLTALQAKAFLLTTCRKLGLAD 300  
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DB 301 IDYTPINNEHLNKEKEEFVNILPTLSNTFSPNPEYKARSGDKAKIMEAKPGYALVGF 360  
QY 360 EISDQSLAVLKVYQAKLKHNQIDKDSLEIVGDIDKLCPPDSEOMYTNKIAFPNEY 419  
DB 361 EISDQSLAVLKVYQAKLKHNQIDKDSLEIVGDIDKLCPPDSEOMYTNKIAFPNEY 420  
QY 420 VITKIAFTYKQLNSLREYEVANFYDSCTGDDIDLNKKKLESSBAEBSMLNANDGVYMPIGT 479  
DB 421 VITKIAFTYKQLNSLREYEVANFYDSCTGDDIDLNKKKLESSBAEBSMLNANDGVYMPIGT 480  
QY 480 ISETFLTPINGFGLVVDENSHLVLTCKSYLRETLATDLSNKKETKLIIPPNGFISNIVE 539  
DB 481 ISETFLTPINGFGLVVDENSHLVLTCKSYLRETLATDLSNKKETKLIIPPNGFISNIVE 540  
QY 540 NGNLEGENLEBWKANNRANVYDHTGNGTGVLYVHEDGESQFISGKALKETIYVQYI 599  
DB 541 NGNLEGENLEBWKANNRANVYDHTGNGTGVLYVHEDGESQFISGKALKETIYVQYI 600  
QY 600 VKGKAAIYLDKDEKNGDIYEETNNLEDPQAVTKRFTITGTSRNVHLIFTSONGERAFGG 659  
DB 601 VKGKAAIYLDKDEKNGDIYEETNNLEDPQAVTKRFTITGTSRNVHLIFTSONGERAFGG 660  
QY 660 NFIISEIRPSEBELISPELINSDAVNSQGTWISGNSINSNVNGTRFONLSLEYSSTYS 719  
DB 661 NFIISEIRPSEBELISPELINSDAVNSQGTWISGNSINSNVNGTRFONLSLEYSSTYS 720

DB 661 NFIISEIRPSEBELISPELINTNNTSGSTHISGNTLTLTYGGRGILKONLQDSFSTYR 720  
QY 720 MNPVNGGKXTINSREVERSYLQESSXYISEKFTTTNNGLVLEISRRAS---RG 776  
DB 721 VYFSVSGDANVRINSRLEVEKGYMS-GADVSEMTTFKPKONFYELISQGNLYGCP 779  
QY 777 VINFGDFSIK 786  
DB 780 IVHFYDYSIK 789

RESULT 6  
US-09-589-477-84  
Sequence 84, Application US/09589477  
Patent No. 6570005  
GENERAL INFORMATION:  
APPLICANT: Schepf, H. Ernest  
APPLICANT: Wicker, Carol  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Walz, Michelle  
APPLICANT: Stochhoff, Brian  
TITLE OF INVENTION: Toxins Active Against Pests  
NUMBER OF SEQUENCES: 105  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Saliwanichik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/589,477  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/886,615  
FILING DATE: 1-JUL-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/674,002  
FILING DATE: 1-JUL-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-701C1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-589-477-84

Query Match 79.6%; Score 3180.5; DB 2; Length 789;  
Best Local Similarity 78.9%; Pred. No. 1.4e-216;  
Matches 623; Conservative 70; Mismatches 92; Indels 5; Gaps 3;

QY 1 MOKNN-KLSYKALPSFIDYNGIYGPATGIDIMNMIFKNTMGDLTDLILKNOQLNE 59  
DB 1 MNNKNTKLSARALPSFIDYNGIYGPATGIDIMNMIFKNTMGDLTDLILKNOQLNE 60  
QY 60 ISGRLDGVNGSLNDLAAQGNLDTELSKEILKIANEONKVLNDVNTKLDAINMLNTYLPK 119  
DB 61 ISGRLDGVNGSLNDLAAQGNLDTELSKEILKIANEONKVLNDVNTKLDAINMLNTYLPK 120

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Db 61 ISGKLDGVNGSLNDLIAQGNINTELSEIKLIANEQNOVLNDVNNKLDAINTMHLIYLPK 120
QY 120 ITSMUSDVWKQNYALGLQIEYLSKOLKEISDKLDIVANNVLIINSTLTETEPAYORIKYVN 179
Db 121 ITSMUSDVWKQNYALSLQIEYLSKOLKEISDKLDIIVANNVLIINSTLTETEPAYORIKYVN 180
QY 180 EKFEALTSATETNLKTQDSSHTDILDELTELTELAKSVTKNDVDGFEFYLTFFHVMIG 239
Db 181 EKFEELTFATETSSKVKDSDPPADILDELTELTELAKSVTKNDVDGFEFYLTFFHVMIG 240
QY 240 NNLFGRSALKTASSELIAKENLKTSGSEGVANNVFLIYLTALQAKAFILTTTCRKLGLAD 299
Db 241 NNLFGRSALKTASSELIAKENVKTSGSEGVANNVFLIYLTALQAKAFILTTTCRKLGLAD 300
QY 300 IDVTPIMNEHLNKEEKEEFVNNILPTLSNTPSNPYEKARGSDKAKIIMEAKGVALVGF 359
Db 301 IDVTSIMNEHLNKEEKEEFVNNILPTLSNTPSNPYAKVKSDEDAKMIYEAAPGVALVGF 360
QY 360 EISKDSIAVLKYVQAKIKHNYQIDKOSLSEIYVGDIDKLLCPDQSEOMYTTNKIAFPNEY 419
Db 361 EWSNDSITVLKYBAKIKQNYOVDKSLSEIYVGDIDKLLCPDQSEQIYTTNNIVFPNEY 420
QY 420 VITKIAFTKLNLSRYEVTANFYDSSGTGDIIDLNKKKTESSEAFESMANNDDGYMPIGT 479
Db 421 VITKIDPTKQAKTLRYEVIANFYDSSGTGDIIDLNKKKTESSEAFRTLSANDDGYMPILGV 480
QY 480 ISETFLTPINGFGLVVDENSRLVLTCKSYLRETLATDLSNKEKTLIVPNGFISNIYE 539
Db 481 ISETFLTPINGFGLQADGNSRLITLTCKSYLRELLATDLSNKEKTLIVPNSGFISNIYE 540
QY 540 NGNLEGENLEPWKANNKAAVYDHTGVNGTKVLYVHEDGFSQFIGDKLKLTKEYVIOYI 599
Db 541 NGSIEEDNLEPWKANNKAAVYDHTGVNGTKVLYVHEDGFSQFIGDKLKLTKEYVIOYI 600
QY 600 VKSKAAIYLKDEKNGDIYEETNNELEDFQAVTKRFTGTDSSRVHLIFTSNGEERAFGG 659
Db 601 VKKSPSILKDEMTGYIHEDTNNNKDYQITTKRFTGTDLKGAVYLLKSGQDEAMGD 660
QY 660 NFIIISIRPSEELLSPELIKSDAMVGSQGTWISGNSININSVNGTFRQNLISSESYTS 719
Db 661 NFIIELISPEKLLSPELIWNMTSTGTHISGNTLTYQGRGLIKQNLQDSDSTYR 720
QY 720 MNNNNGFGKVTIRNSREVVEFSYLOFSKYSISEKFTTTTNTGTYELSRASS--RG 776
Db 721 VYFSVGDANVLRIRNSREVLFEKGYS- GAKDVSEMTTKFEKONFYIELSQNNLNYGCG 779
QY 777 VINFGDSIK 786
Db 780 IYHFYVDSIK 789

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RESULT 7  
 US-10-099-285A-84  
 ; Sequence 84, Application us/10099285A  
 ; Patent No. 6752992

## GENERAL INFORMATION:

APPLICANT: Schmeff, H. Ernest  
 Wicker, Carol  
 Narva, Kenneth E.  
 Walz, Michelle  
 Stockhoff, Brian  
 Muller-Cohn, Judy  
 TITLE OF INVENTION: Toxins Active Against Pests  
 NUMBER OF SEQUENCES: 105  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: Florida  
 COUNTRY: USA  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/099,285A
/ FILING DATE: 02-Jul-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 09/002,285
/ FILING DATE: 31-DEC-1997
/ APPLICATION NUMBER: US 08/886,615
/ FILING DATE: 1-JUL-1997
/ APPLICATION NUMBER: US 08/674,002
/ FILING DATE: 1-JUL-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sanders, Jay M.
/ REGISTRATION NUMBER: 39,355
/ REFERENCE/DOCKET NUMBER: MA-701C2D1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (352) 375-8100
/ TELEFAX: (352) 372-5800
/ INFORMATION FOR SEQ ID NO: 84:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 789 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-099-285A-84

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Query Match 79.6%; Score 3180.5; DB 2; Length 789;

Best Local Similarity 78.9%; Pred. No. 1.4e-216;

Matches 623; Conservative 70; Mismatches 92; Indels 5; Gaps 3;

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QY 1 MOKNN-KLSVKAIPSIDYFNIGYGFATGKIDIMNMIFFKNTGGDTLDEILKNQOLNE 59
Db 1 MNKNNTKLSARALPSRIDYFNIGYGFATGKIDIMNMIFFKNTGGDTLDEILKNQOLNE 60
QY 60 ISGKLDGVNGSLNDLIAQGNINTELSEIKLIANEQNOVLNDVNNKLDAINTMHLIYLPK 119
Db 61 ISGKLDGVNGSLNDLIAQGNINTELSEIKLIANEQNOVLNDVNNKLDAINTMHLIYLPK 120
QY 120 ITSMUSDVWKQNYALGLQIEYLSKOLKEISDKLDIVANNVLIINSTLTETEPAYORIKYVN 179
Db 121 ITSMUSDVWKQNYALSLQIEYLSKOLKEISDKLDIIVANNVLIINSTLTETEPAYORIKYVN 180
QY 180 EKFEALTSATETNLKTQDSSHTDILDELTELTELAKSVTKNDVDGFEFYLTFFHVMIG 239
Db 181 EKFEELTFATETSSKVKDSDPPADILDELTELTELAKSVTKNDVDGFEFYLTFFHVMIG 240
QY 240 NNLFGRSALKTASSELIAKENLKTSGSEGVANNVFLIYLTALQAKAFILTTTCRKLGLAD 299
Db 241 NNLFGRSALKTASSELIAKENVKTSGSEGVANNVFLIYLTALQAKAFILTTTCRKLGLAD 300
QY 300 IDVTPIMNEHLNKEEKEEFVNNILPTLSNTPSNPYEKARGSDKAKIIMEAKGVALVGF 359
Db 301 IDVTSIMNEHLNKEEKEEFVNNILPTLSNTPSNPYAKVKSDEDAKMIYEAAPGVALVGF 360
QY 360 EISKDSIAVLKYVQAKIKHNYQIDKOSLSEIYVGDIDKLLCPDQSEOMYTTNKIAFPNEY 419
Db 361 EWSNDSITVLKYBAKIKQNYOVDKSLSEIYVGDIDKLLCPDQSEQIYTTNNIVFPNEY 420
QY 420 VITKIAFTKLNLSRYEVTANFYDSSGTGDIIDLNKKKTESSEAFESMANNDDGYMPIGT 479
Db 421 VITKIDPTKQAKTLRYEVIANFYDSSGTGDIIDLNKKKTESSEAFRTLSANDDGYMPILGV 480
QY 480 ISETFLTPINGFGLVVDENSRLVLTCKSYLRETLATDLSNKEKTLIVPNGFISNIYE 539
Db 481 ISETFLTPINGFGLQADGNSRLITLTCKSYLRELLATDLSNKEKTLIVPNSGFISNIYE 540
QY 540 NGNLEGENLEPWKANNKAAVYDHTGVNGTKVLYVHEDGFSQFIGDKLKLTKEYVIOYI 599

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Db 541 NGSEEDNLEBPKANNKNAAYVDHTGVNGTKALVYHKDGGFSGPFGDKLKEETEVLOYT 600  
Qy 600 VKGAAYLTKDEKNGDYIYEETNNLEDFQAVTKRFTTGDSRVHLIFTSONGEBAFG 659  
Db 601 VKGPRSHLKDEBNGYIHYEDTNNLKDYOITTKRFTTGDKGVYLLKSONGDEAWGD 660  
Qy 660 NFIISEIRPSEBELLSPELIKSDAWVSGQWTWISGNSLNINSVNGTFRONLSLESTYS 719  
Db 661 NFIILEISPSBKLSPELINTNNMTSTGTHISGNTLTLVQGGRIKLQNLQDLSFSTYR 720  
Qy 720 MNFVNGFGKVTIRNSREVVERSYLOFSKYSIKSEKFTTTNNGLVYELSRASS--RG 776  
Db 721 VYFVSVDANVRIRNSREVLPEKGYMS-GADVSEMFTTKBKONFYIELSQGNLYGAP 779  
Qy 777 VINFDFPSIK 786  
Db 780 IVHFYDVSIX 789

RESULT 8  
US-09-002-285-92  
; Sequence 92, Application US/09002285  
; Patent No. 6369213  
; GENERAL INFORMATION:  
; APPLICANT: Schnepf, H. Ernest  
; APPLICANT: Wicker, Carol  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Walz, Michelle  
; APPLICANT: Stockhoff, Brian  
; APPLICANT: Muller-Cohn, Judy  
; TITLE OF INVENTION: Toxins Active Against Pests  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Saliwanchik, Lloyd & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/002,285  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/886,615  
; FILING DATE: 1-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/674,002  
; FILING DATE: 1-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sanders, Jay M.  
; REGISTRATION NUMBER: 39,355  
; REFERENCE/DOCKET NUMBER: MA-701C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 92:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 789 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-002-285-92

Query Match 79.5%; Score 3176.5; DB 2; Length 789;  
Best Local Similarity 78.9%; Pred. No. 2.6e-216;  
Matches 623; Conservative 69; Mismatches 93; Indels 5; Gaps 3;

Qy 1 MOKAN-KLSVKALPSFIDYFNGIYGPATGIDIMNMIKFTNTGGDLTLDEILKNQOOLNE 59  
Db 1 MKNKNTKLSAPALBSFIDYFNGIYGPATGIDIMNMIKFTDTGGNLTLDEILKNQOOLNE 60  
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Db 61 ISGLDGVNGSLNDLLAQGNLDELKREILKIANEONQVANDVNNKLDALINMLHTYLPK 120  
Qy 120 ITSMLSVDMKONVALSLQIEYLSKQLEISPKLDIVINVTILNSTLREITPAYORIKYVN 179  
Db 121 ITSMLSVDMKONVALSLQIEYLSKQLEISPKLDIINNVTILNSTLREITPAYORIKYVN 180  
Qy 180 EKFEALTSATEYNLKTQDSSHTDILDELTELTELASVTKNQDVGFEFYANTFHWVIG 239  
Db 181 EKFEELTPATYTTTLKVKDSSPADILDELTELTELASVTKNQDVGFEFYANTFHWVIG 240  
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Db 241 NNLFGRSALKTASELAKENKVTSGSEVGVNVEFLVLTALQAKAPLTLTTCRLKLGAD 300  
Qy 300 IDYTPINMEHLNKEKEFRVNIILPTLSNTSNPNYERAKGSDKAKIIMEAKPGYALVF 359  
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Qy 360 EISKDSIAYLKVYQAKLKHNQIDKDSLSEIVYGDIDKLCPDQSEOMYYTNKIAFPNEY 419  
Db 361 EKSNDSTIVLKVYPAKLIKONQVNDKSLSEVYIGDTKLCPDQSEQYITNNIVFNEY 420  
Qy 420 VITKIAPTKLNSLRVEVTANFYDSSTGDIIDLNKKLESSEAEFSMLNANDGYMPDGT 479  
Db 421 VITKIDPTKMKTLRYEVTANFYDSSGGEIDLNKKYESSAEYRTLSANDGYMPDGV 480  
Qy 480 ISEFTFLPPIGFGVLVDENGRVLTCKSYRRETLATDLSNKKTKLIVPNGTISNVE 539  
Db 481 ISEFTFLPPIGFGVLQADGNSRLITLTKSYRRETLATDLSNKKTKLIVPSPGISNVE 540  
Qy 540 NGNLEGNLEBPKANNKNAAYVDHTGVNGTKVLYVHDEGSPFIDGDKLKEETEVLOYT 599  
Db 541 NGSEEDNLEBPKANNKNAAYVDHTGVNGTKALVYHKDGGIISOPFGDKLKEETEVLOYT 600  
Qy 600 VKGAAYLTKDEKNGDYIYEETNNLEDFQAVTKRFTTGDSRVHLIFTSONGEBAFG 659  
Db 601 VKGPRSHLKDEBNGYIHYEDTNNLKDYOITTKRFTTGDKGVYLLKSONGDEAWGD 660  
Qy 660 NFIISEIRPSEBELLSPELIKSDAWVSGQWTWISGNSLNINSVNGTFRONLSLESTYS 719  
Db 661 NFIILEISPSBKLSPELINTNNMTSTGTHISGNTLTLVQGGRIKLQNLQDLSFSTYR 720  
Qy 720 MNFVNGFGKVTIRNSREVVERSYLOFSKYSIKSEKFTTTNNGLVYELSRASS--RG 776  
Db 721 VYFVSVDANVRIRNSREVLPEKGYMS-GADVSEMFTTKBKONFYIELSQGNLYGAP 779  
Qy 777 VINFDFPSIK 786  
Db 780 IVHFYDVSIX 789

RESULT 9  
US-09-589-477-92  
; Sequence 92, Application US/09589477  
; Patent No. 6570005  
; GENERAL INFORMATION:  
; APPLICANT: Schnepf, H. Ernest  
; APPLICANT: Wicker, Carol  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Walz, Michelle  
; APPLICANT: Stockhoff, Brian  
; TITLE OF INVENTION: Toxins Active Against Pests  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Saliwanchik, Lloyd & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1

```

CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,477
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-589-477-92

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Query Match 79.5%; Score 3176.5; DB 2; Length 789;

Best Local Similarity 78.9%; Pred. No. 2.6e-216;

Matches 623; Conservative 69; Mismatches 93; Indels 5; Gaps 3;

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QY 1 MOKN-KLSYKALPSFDYNGYIGRTGDKIMNMIFKNTGDLTLDEILKNOOLNE 59
DB 1 MNKNNTKLSARALPSFDYNGYIGRTGDKIMNMIFKNTGDLTLDEILKNOOLNE 60
QY 60 ISGKLDGVNGLNDLLAOGNLDTLSKEIKIANEONKVANDNTKLDATNMLNTYLPK 119
DB 61 ISGKLDGVNGLNDLLAOGNLDTLSKEIKIANEONKVANDNTKLDATNMLNTYLPK 120
QY 120 ITSMUSDVKNQYALGLQIEYLSKQKEISDKLDVINNVNLINSTLTETPAYORIKYVN 179
DB 121 ITSMUSDVKNQYALGLQIEYLSKQKEISDKLDVINNVNLINSTLTETPAYORIKYVN 180
QY 180 EKEEALTSATETMLTKKODSSHDIIDELTELTELAKSVTKNDVDFEFLNTFHDVVG 239
DB 181 EKEEALTSATETMLTKKODSSHDIIDELTELTELAKSVTKNDVDFEFLNTFHDVVG 240
QY 240 NNLFGRSALKTASELAKENLKTSGSEVGVNVLIVLFLAOKAFLLTTCRKLGLAD 299
DB 241 NNLFGRSALKTASELAKENLKTSGSEVGVNVLIVLFLAOKAFLLTTCRKLGLAD 300
QY 300 IDYTPIMNEHLNKEEKEFRVNIPLTSLNFSNPNYKARQSDKAKIMEAKPGVALVGF 359
DB 301 IDYTPIMNEHLNKEEKEFRVNIPLTSLNFSNPNYKARQSDKAKIMEAKPGVALVGF 360
QY 360 ELSKSDIAVLKYQAQLKKNYQDKDSLSRIYVGDIDKILCPQOSQMTYTKIAPNEY 419
DB 361 ELSKSDIAVLKYQAQLKKNYQDKDSLSRIYVGDIDKILCPQOSQMTYTKIAPNEY 420
QY 420 VITKIAFTKILNSLREYEVANFYDSSTGDIIDLNKKKIESSEAFSMLNANNQGVVPIGT 479
DB 421 VITKIDFTKIMTLRIEVTANFYDSSTGDIIDLNKKKIESSEAFSMLNANNQGVVPIGT 480

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QY 480 ISETFLPINGFGLVVDENSLVTLFCKSYLRETLATDLSNKEKTLIVPPNGFISNIVE 539
DB 481 ISETFLPINGFGLVVDENSLVTLFCKSYLRETLATDLSNKEKTLIVPPNGFISNIVE 540
QY 540 NGNIEGENLEPMKANNKNAVYDHTGVNGTKVLYVHEDGFPSQFIDKLTAKTEYVIOYI 599
DB 541 NGNIEEDNLEPMKANNKNAVYDHTGVNGTKVLYVHEDGFPSQFIDKLTAKTEYVIOYI 600
QY 600 VKGKAAYIKDENKNGDIYETETNELEDPOAVTKRFLITGDSRVHLIFTSQGEARFG 659
DB 601 VKGKPSIHLKDEYNGYIHYEDTNNLNKYQITTKRFTTGIDLGAVYILKLSQNGDEAMGD 660
QY 660 NFIISEIRPSEELISPELISDAMVGSQGTWISGNSININSVNGTFPRONLSSEYSTYS 719
DB 661 NFIISEIRPSEELISPELISDAMVGSQGTWISGNSININSVNGTFPRONLSSEYSTYS 720
QY 720 MNFNVNGFGKVTIRNSREVEFRSYLQFSSKYSIEKFTTTNNNGLYVELSRAS--RG 776
DB 721 VYFVSQGDANVIRNSREVEFRSYLQFSSKYSIEKFTTTNNNGLYVELSRAS--RG 779
QY 777 VINFGPESIK 786
DB 780 VHFYDVSIX 789

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# RESULT 10

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US-10-099-285A-92
Sequence 92, Application US/10099285A
Patent No. 6752992
GENERAL INFORMATION:
APPLICANT: Schnerf, H. Ernest
Wicker, Carol
Narva, Kenneth E.
Walz, Michelle
Stoekhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285A
FILING DATE: 02-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/002,285
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 amino acids
TYPE: amino acid
STRANDEDNESS: single

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Db 301 IDYTSIMNEHLNKEKEEFVNILPTLSNTFSNPNYAKVGSDEDAKMIVEAKPGHALIGF 360  
Qy 360 EISKDSIAVLKYQAKLKHNYQIDKDSISEIYVGIDKLCPODSEOMYTNKIAFPNEY 419  
Db 361 EISNDSITVLKYAEAKLKONQVDDKDSIEVIYGDMDKLCPPDSEQIYTNINIVFPNEY 420  
Qy 420 VITKIAFTKLNLSRYEVTANFYDSTGDIIDLNKKKIESSEAFESMLNANNGVYMPIGT 479  
Db 421 VITKIDFTKMKTLRYEVTANFYDSTGDIIDLNKKKVESSEAFERTLSANDGVYMPIGV 480  
Qy 480 ISETFLTPINGFGLVVDENSRVLTLTKSYARELLATDLSNKKTKLIYPPNGFISNIYE 539  
Db 481 ISETFLTPINGFGLQADENSRVLTLTKSYARELLATDLSNKKTKLIYPPNGFISNIYE 540  
Qy 540 NGNLEGENLEPWKANNKAAVYDHTGVNGTKVLYVHDEGEFSGFIDGKUKLKTETEVYQYI 599  
Db 541 NGSTIEDNLEPWKANNKAAVYDHTGVNGTKVLYVHDEGGSQFIDGKUKLKTETEVYQYT 600  
Qy 600 VKGKAIIYLKDEKNGDYIYEETNNELEDFQAVTKRFTGTDSRVHLIFTSONGEBAFGG 659  
Db 601 VKGKPSIHLKDENGTYIHYEDTNNLEDTYQINRKFPTGTDLKGVYLIILKSQNGDEAMGD 660  
Qy 660 NFIISEIRPSEELLSPELISKSDAWVSGQGTWISGNSLINSNVNGTFRONLSLESYSTYS 719  
Db 661 NFIILEISPEKLLSPELINTNMTSTGSTNISGNTLTLTYQGGRGILKONQLODSFSTYR 720  
Qy 720 MNFNNGFGKVTIRNSREVFERSYLOFSSKYISEKFTYTNNTGLVVELSRASS---RG 776  
Db 721 VYFSVSDANVRIRNSREVFERSYLOFSSKYISEKFTYTNNTGLVVELSRASS---RG 779  
Qy 777 VINFGPSIK 786  
Db 780 IVHFYDVSIR 789

RESULT 12  
US-09-073-898-8  
Sequence 8, Application US/09073898  
Patent No. 6242669  
GENERAL INFORMATION:  
APPLICANT: Feltelson, Gerald S.  
APPLICANT: Schnepf, H. Ernest  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Stockhoff, Brian A.  
APPLICANT: Schmeltz, James  
APPLICANT: Loewer, David  
APPLICANT: Dullum, Charles Joseph  
APPLICANT: Muller-Cohn, Judy  
APPLICANT: Stamp, Lisa  
APPLICANT: Morrill, George  
APPLICANT: Finstad-Lee, Stacey  
TITLE OF INVENTION: No. 6242669el Pepticidal Toxins and Nucleotide  
TITLE OF INVENTION: Sequences which Encode These Toxins  
NUMBER OF SEQUENCES: 144  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/073,898  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/960,780  
FILING DATE: 30-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-708C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 790 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Jav90  
US-09-073-898-8

Query Match 79.5%; Score 3175.5; DB 2; Length 790;  
Best Local Similarity 78.6%; Pred. No. 3,1e-216;  
Matches 621; Conservative 70; Mismatches 94; Indels 5; Gaps 3;

Qy 1 MOKN-KLSYKALPSFIDYFNNGIYGFATGKIDIMNMFKTNTGDTLTDEILKNOOLNE 59  
Db 1 MNKNKTLSTRALPSFIDYFNNGIYGFATGKIDIMNMFKTNTGDTLTDEILKNOOLNE 60  
Qy 60 ISGKLDGVNGSLNDLLAOGNLDTELSEKILKIANEQNKYLVDPNTGLDAINMLNTYLPK 119  
Db 61 ISGKLDGVNGSLNDLLAOGNLTDELSEKILKIANEQNKYLVDPNTGLDAINMLNTYLPK 120  
Qy 120 ITSMUSDVWKONALGLQIEYLSKOLKEISDKLDVINAVNLINSTLTBITPAYORIKYVN 179  
Db 121 ITSMUSDVWKONALGLQIEYLSKOLKEISDKLDVINAVNLINSTLTBITPAYORIKYVN 180  
Qy 180 EKFEALTSATETNMLTKKODSSHTDIDELTELTELAKSTYKNDVDFEFTYNTFHVVMG 239  
Db 181 EKFEALTSATETNMLTKKODSSHTDIDELTELTELAKSTYKNDVDFEFTYNTFHVVMG 240  
Qy 240 NMLFGSALKTASELIAKENLKTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLAD 299  
Db 241 NMLFGSALKTASELITKENNVTSSEGVNPNFLIVLTALQAKAFLLTTCRKLGLAD 300  
Qy 300 IDYTPIMNEHLNKEKEEFVNILPTLSNTFSNPNTEKARGSXDAKIINEARPGVALYGF 359  
Db 301 IDYTSIMNEHLNKEKEEFVNILPTLSNTFSNPNYAKVGSDEDAKMIVEAKPGHALIGF 360  
Qy 360 EISKDSIAVLKYQAKLKHNYQIDKDSISEIYVGIDKLCPODSEOMYTNKIAFPNEY 419  
Db 361 EISNDSITVLKYAEAKLKONQVDDKDSIEVIYGDMDKLCPPDSEQIYTNINIVFPNEY 420  
Qy 420 VITKIAFTKLNLSRYEVTANFYDSTGDIIDLNKKKIESSEAFESMLNANNGVYMPIGT 479  
Db 421 VITKIDFTKMKTLRYEVTANFYDSTGDIIDLNKKKVESSEAFERTLSANDGVYMPIGV 480  
Qy 480 ISETFLTPINGFGLVVDENSRVLTLTKSYARELLATDLSNKKTKLIYPPNGFISNIYE 539  
Db 481 ISETFLTPINGFGLQADENSRVLTLTKSYARELLATDLSNKKTKLIYPPNGFISNIYE 540  
Qy 540 NGNLEGENLEPWKANNKAAVYDHTGVNGTKVLYVHDEGEFSGFIDGKUKLKTETEVYQYI 599  
Db 541 NGSTIEDNLEPWKANNKAAVYDHTGVNGTKVLYVHDEGGSQFIDGKUKLKTETEVYQYT 600  
Qy 600 VKGKAIIYLKDEKNGDYIYEETNNELEDFQAVTKRFTGTDSRVHLIFTSONGEBAFGG 659  
Db 601 VKGKPSIHLKDENGTYIHYEDTNNLEDTYQINRKFPTGTDLKGVYLIILKSQNGDEAMGD 660  
Qy 660 NFIISEIRPSEELLSPELISKSDAWVSGQGTWISGNSLINSNVNGTFRONLSLESYSTYS 719  
Db 661 NFIILEISPEKLLSPELINTNMTSTGSTNISGNTLTLTYQGGRGILKONQLODSFSTYR 720

Qy 720 MNFVNGFGKVTIRNSREVVERSYLOFSSKYISEKFTTTNNGLVYELSRASS---RG 776  
Db 721 VYFVSQGANVRIRNSREVLFKRYMS-GAKDVSEMTTKREKONFYIELSQGNLVGCP 779

Qy 777 VINFGPSIK 786  
Db 780 IVHFYDVSIK 789

## RESULT 13

US-09-307-106-2  
Sequence 2, Application US/09307106  
Patent No. 6603063  
GENERAL INFORMATION:  
APPLICANT: Fetteleson, Jerald S.  
APPLICANT: Schnepf, H. Ernest  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Stockhoff, Brian A.  
APPLICANT: Schneits, James  
APPLICANT: Loewer, David  
APPLICANT: Dullum, Charles Joseph  
APPLICANT: Muller-Cohn, Judy  
APPLICANT: Stamp, Lisa  
APPLICANT: Morrill, George  
APPLICANT: Finstad-Lee, Stacey  
TITLE OF INVENTION: No. 6603063el Pesticidal Toxins and Nucleotide  
TITLE OF INVENTION: Sequences Which Encode These Toxins  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/307,106  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/960,780  
FILING DATE: 30-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/073,898  
FILING DATE: 05-MAY-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-708C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 790 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Jay90  
US-09-307-106-2

Query Match 79.5%; Score 3175.5; DB 2; Length 790;  
Best Local Similarity 78.6%; Pred. No. 3.1e-216;

Matches 621; Conservative 70; Mismatches 94; Indels 5; Gaps 3;

Qy 1 MOKN-ELSVKALPSFIDYNGYGFATGKIDIMNMFKNTGGDLTLDELKNOQLNE 59  
Db 1 MNKNYTLSTRALPSFIDYNGYGFATGKIDIMNMFKNTGGDLTLDELKNOQLNE 60  
Qy 60 ISGKLDGVSINDLAQGNLDTELSEIKIANEQKRVANDVTKDAINLMNTYLPK 119  
Db 61 ISGKLDGVSINDLAQGNLDTELSEIKIANEQKRVANDVTKDAINLMNTYLPK 120  
Qy 120 ITSMUSDVMTKNTALGLQIEYLSKOLKEISDKLDVINNVNLINSTLETIPAYORIKYVN 179  
Db 121 ITSMUSDVMTKNTALGLQIEYLSKOLKEISDKLDVINNVNLINSTLETIPAYORIKYVN 180  
Qy 180 EKFEALTSATETNKTDQSSHDHLDLTELTELASVTKNDVGEFYNTHFDWIG 239  
Db 181 EKFEALTSATETNKTDQSSHDHLDLTELTELASVTKNDVGEFYNTHFDWIG 240  
Qy 240 NNLFGRSALKTASBLIKENILKTSSEVGVNPNFLVLTALQAKAPLTLTCRKLGLAD 299  
Db 241 NNLFGRSALKTASBLIKENILKTSSEVGVNPNFLVLTALQAKAPLTLTCRKLGLAD 300  
Qy 300 IDYTPINNEHLNKEKEEFVNVILPTLSNTESNPYERKAGSDKDAKIMEAKPGYALVGF 359  
Db 301 IDYTSINNEHLNKEKEEFVNVILPTLSNTESNPYERKAGSDKDAKIMEAKPGYALVGF 360  
Qy 360 EISKDSIYAVLYKYQAKIKHNYQDKSLSEIVYGDIDKLCPPQSEDMYTTNKIAFNEY 419  
Db 361 EISKDSIYAVLYKYQAKIKHNYQDKSLSEIVYGDIDKLCPPQSEDMYTTNKIAFNEY 420  
Qy 420 VITKIAFTKKNLSRYEVTANFYDSSYTGDIIDLNKCKIESSEAEPSMLNANDGVMPYIGT 479  
Db 421 VITKIDTCKMKTIRYEVTVANFYDSSYTGDIIDLNKCKIESSEAEPSMLNANDGVMPYIGT 480  
Qy 480 ISETFLTPINGFGLVDENSRLVTLTKCSYLRETLATDLSNKEFKLIVPNGFISNIVE 539  
Db 481 ISETFLTPINGFGLVDENSRLVTLTKCSYLRETLATDLSNKEFKLIVPNGFISNIVE 540  
Qy 540 NGNLEGNLEPWRKANNNAVVDHTGNGKRLVYHEDGFSPQFGKLLKTEYVVOYI 599  
Db 541 NGNLEGNLEPWRKANNNAVVDHTGNGKRLVYHEDGFSPQFGKLLKTEYVVOYI 600  
Qy 600 VKGKAIFYLDEKNGDIYEETNNELEDFOAVTKRFTTGDSRVHLIFTSQNEBEAFGG 659  
Db 601 VKGKPSIHLDEKNGDIYEETNNELEDFOAVTKRFTTGDSRVHLIFTSQNEBEAFGG 660  
Qy 660 NFIISEIRPSEBELISPELISDAMVGSQGTWISGNSLINSNVNGFRQMLSESYSTYS 719  
Db 661 NFIISEIRPSEBELISPELISDAMVGSQGTWISGNSLINSNVNGFRQMLSESYSTYS 720  
Qy 720 MNFVNGFGKVTIRNSREVVERSYLOFSSKYISEKFTTTNNGLVYELSRASS---RG 776  
Db 721 VYFVSQGANVRIRNSREVLFKRYMS-GAKDVSEMTTKREKONFYIELSQGNLVGCP 779

## RESULT 14

US-09-850-351A-8  
Sequence 8, Application US/09850351A  
Patent No. 6656908  
GENERAL INFORMATION:  
APPLICANT: Fetteleson, Jerald S.  
APPLICANT: Schnepf, H. Ernest  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Stockhoff, Brian A.  
APPLICANT: Schneits, James  
APPLICANT: Loewer, David  
APPLICANT: Dullum, Charles Joseph  
APPLICANT: Muller-Cohn, Judy  
APPLICANT: Stamp, Lisa



APPLICATION NUMBER: US 08/037,057  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: P-40,403  
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV7 - SOLV3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8582  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-471-033-29

Query Match 79.4%; Score 3171.5; DB 1; Length 789;

Best Local Similarity 78.5%; Pred. No. 66-216;  
Matches 620; Conservative 71; Mismatches 94; Indels 5; Gaps 3;

QY 1 MOKN-KLSYKALPSFIDYFNGIYGFATGIDIMNMIFKNTGGDLTLDLTKNOQLNE 59  
DB 1 MNKNITLSTRALPSFIDYFNGIYGFATGIDIMNMIFKIDTGGDLTLDLTKNOQLND 60  
QY 60 ISGLDGVNSLNDLDAQNDTELSEIKLIANEONKVLNDVNTKLDATNMTYLPK 119  
DB 61 ISGLDGVNSLNDLDAQNDTELSEIKLIANEONKVLNDVNTKLDATNMTYLPK 120  
QY 120 ITSMUSDVMOQNALGLQIEYLSKOLKEISDKLDVINNVNLNSTLEITPAYORIKYVN 179  
DB 121 ITSMUSDVMOQNALGLQIEYLSKOLKEISDKLDVINNVNLNSTLEITPAYORIKYVN 180  
QY 180 EKPEALTSATEMUKTQDSHNDLDBLTELTLAKSVTKNDVDFEFTYNTFHDVMTG 239  
DB 181 EKPEALTSATEMUKTQDSHNDLDBLTELTLAKSVTKNDVDFEFTYNTFHDVMTG 240  
QY 240 NNLFGRSALKTASLAKENLKTSGSEVGVNPNFLIVLTALQAKFLITTCRKLGLAD 299  
DB 241 NNLFGRSALKTASLAKENLKTSGSEVGVNPNFLIVLTALQAKFLITTCRKLGLAD 300  
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DB 301 IDYTPINNEHLNKEKEFRVNIILPTLSNTSPNRYEKARGSDKAKIMEAKPGVALVGF 360  
QY 360 EISDQSLAVLKVYQAKIKANYQIDKSLSEIVYGDIDKLCPDQSEQMYTNNKIAPNEY 419  
DB 361 EISDQSLAVLKVYQAKIKANYQIDKSLSEIVYGDIDKLCPDQSEQMYTNNKIAPNEY 420  
QY 420 VITKIAFTKLNLSRYEVTANFVDSSTGDDIDNKKKIESSEAEFSMTNANDGYMPIGT 479  
DB 421 VITKIDFTKLNLSRYEVTANFVDSSTGDDIDNKKKIESSEAEFSMTNANDGYMPIGT 480  
QY 480 ISETFLTPINGFGIIVDENSRLVTLTCKSYLRETLATDLSNKETKLIIPPNGFISNIVE 539  
DB 481 ISETFLTPINGFGIIVDENSRLVTLTCKSYLRETLATDLSNKETKLIIPPNGFISNIVE 540  
QY 540 NGNLEGENLEPWKANNQAYVDHTGVNGTKVLYVHEDGEPQFIDGKLKTEYVIOYT 599  
DB 541 NGNLEGENLEPWKANNQAYVDHTGVNGTKVLYVHEDGEPQFIDGKLKTEYVIOYT 600  
QY 600 VKGKAAYLDEKNGDVIYEETNNLEDPQAVTKRFITGTDSSRVHLIFTSQNGEAPAGG 659  
DB 601 VKGKAAYLDEKNGDVIYEETNNLEDPQAVTKRFITGTDSSRVHLIFTSQNGEAPAGG 660  
QY 660 NFIISIRPSEBELSPELIKSDAVVSGQTWISGNSLINSNVNTPRONLSLESYSTYS 719  
DB 661 NFIISIRPSEBELSPELIKSDAVVSGQTWISGNSLINSNVNTPRONLSLESYSTYS 720  
QY 720 MNRVNGFGKVTITNSREVVFERSYLOFSSKVIYSEKFTTTNTGTYVELSPASS--RG 776  
DB 721 MNRVNGFGKVTITNSREVVFERSYLOFSSKVIYSEKFTTTNTGTYVELSPASS--RG 777

QY 777 VINQDFPSIK 786  
DB 780 IVHFYDVSIX 789

Search completed: May 15, 2006, 20:44:55  
Job time : 50 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 15, 2006, 20:44:16 ; Search time 168 Seconds  
(without alignments)  
1954.844 Million cell updates/sec

Title: US-10-698-096-17  
Perfect score: 3995  
Sequence: 1 MQNNKLSVYALPSFIDYFN.....VELSRASSRGVINFQPSIK 786

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.Main:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3995	100.0	786	4	US-10-698-096-17 Sequence 17, Appl
2	3507.5	87.8	787	4	US-10-473-687-2 Sequence 2, Appl
3	3507.5	87.8	787	5	US-10-505-315-7 Sequence 7, Appl
4	3505	87.7	787	4	US-10-452-002A-54 Sequence 54, Appl
5	3505	87.7	787	4	US-10-698-096-25 Sequence 25, Appl
6	3505	87.7	788	4	US-10-698-096-27 Sequence 27, Appl
7	3499.5	87.6	787	4	US-10-473-687-7 Sequence 7, Appl
8	3243.5	81.2	788	5	US-10-505-315-32 Sequence 32, Appl
9	3239	81.1	788	5	US-10-505-315-2 Sequence 2, Appl
10	3235	81.0	788	5	US-10-505-315-11 Sequence 11, Appl
11	3182.5	79.7	789	4	US-10-099-285-82 Sequence 82, Appl
12	3180.5	79.6	789	4	US-10-099-285-84 Sequence 84, Appl
13	3176.5	79.5	789	4	US-10-099-285-92 Sequence 92, Appl
14	3175.5	79.5	789	4	US-10-473-687-5 Sequence 5, Appl
15	3175.5	79.5	789	5	US-10-505-315-5 Sequence 5, Appl
16	3175.5	79.5	790	3	US-09-850-351A-8 Sequence 8, Appl
17	3175.5	79.5	790	4	US-10-452-002A-2 Sequence 2, Appl
18	3175.5	79.5	790	4	US-10-698-096-8 Sequence 8, Appl
19	3172.5	79.4	786	4	US-10-698-096-19 Sequence 19, Appl
20	3171.5	79.4	789	3	US-09-904-226-2 Sequence 2, Appl
21	3170.5	79.4	789	4	US-10-099-285-78 Sequence 78, Appl
22	3170.5	79.4	789	4	US-10-099-285-94 Sequence 94, Appl
23	3170.5	79.4	789	4	US-10-099-285-96 Sequence 96, Appl
24	3167.5	79.3	789	3	US-09-850-351A-6 Sequence 6, Appl
25	3167.5	79.3	789	4	US-10-698-096-6 Sequence 6, Appl
26	3158.5	79.1	790	3	US-09-850-351A-4 Sequence 4, Appl
27	3158.5	79.1	790	4	US-10-698-096-4 Sequence 4, Appl

28	3156.5	79.0	789	3	US-09-904-226-4 Sequence 4, Appl
29	3151	78.9	790	4	US-10-099-285-102 Sequence 102, App
30	3149.5	78.8	789	4	US-10-099-285-98 Sequence 98, Appl
31	3132.5	78.4	789	4	US-10-099-285-90 Sequence 90, Appl
32	3130.5	78.4	789	4	US-10-099-285-100 Sequence 100, App
33	3083.5	77.2	789	4	US-10-099-285-80 Sequence 80, Appl
34	3073.5	76.9	746	3	US-09-904-226-6 Sequence 6, Appl
35	2423.5	60.7	759	4	US-10-099-285-86 Sequence 86, Appl
36	2405.5	60.2	801	5	US-10-505-315-9 Sequence 9, Appl
37	2233	55.9	511	4	US-10-099-285-88 Sequence 8, Appl
38	208.5	5.2	2539	5	US-10-831-070-6 Sequence 6, Appl
39	205.5	5.1	2265	4	US-10-282-122A-45123 Sequence 45123, A
40	203.5	5.1	1315	5	US-10-744-672-5 Sequence 5, Appl
41	203.5	5.1	1315	5	US-10-744-616-5 Sequence 5, Appl
42	203.5	5.1	1315	5	US-10-470-048B-124 Sequence 124, App
43	195.5	4.9	3533	4	US-10-282-122A-70177 Sequence 70177, A
44	194.5	4.9	1349	3	US-09-815-242-5898 Sequence 5898, Ap
45	194.5	4.9	1349	3	US-09-815-242-13137 Sequence 13137, A

## ALIGNMENTS

```
RESULT 1
US-10-698-096-17
; Sequence 17, Application US/10698096
; Publication No. US20040128716A1
; GENERAL INFORMATION:
; APPLICANT: Narva, Kenneth
; TITLE OF INVENTION: Polynucleotides, Pesticidal Proteins, and Novel Methods of Using
; FILE REFERENCE: MA-708C0C1
; CURRENT FILING DATE: 2003-10-31
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 09/850,351
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 09/073,898
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 08/690,780
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,848
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-698-096-17

Query Match      100.0%; Score 3995; DB 4; Length 786;
Best Local Similarity 100.0%; Pred. No. 1.1e-236;
Matches 786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MQNNKLSVYALPSFIDYFNIGYGFANGLKDIWNMI FKNITGSDLTLDLTKNOQLNRI 60
      |||
DB      1  MQNNKLSVYALPSFIDYFNIGYGFANGLKDIWNMI FKNITGSDLTLDLTKNOQLNRI 60
      |||

QY      61  SGRLDVGNSLNDLDAQNLDTLSKEILKIANEQKRVNDVTKLDAINLMNTYLPKI 120
      |||
DB      61  SGRLDVGNSLNDLDAQNLDTLSKEILKIANEQKRVNDVTKLDAINLMNTYLPKI 120
      |||

QY      121 TSWLSVDMKONVYALGIQIEYLSQQLKEISDKLDVINNVNLINSTLTETIPAYORIKYNE 180
      |||
DB      121 TSWLSVDMKONVYALGIQIEYLSQQLKEISDKLDVINNVNLINSTLTETIPAYORIKYNE 180
      |||

QY      181 KPEALTSATRETNKTKQDSSHTDILDELTELTAQSVTKNDVGEFYLNTFHDWIGN 240
      |||
DB      181 KPEALTSATRETNKTKQDSSHTDILDELTELTAQSVTKNDVGEFYLNTFHDWIGN 240
      |||

QY      241 NLFGRSALTYASLTIKENLKTSGSEVGNVNFLLVTLALQAKAFLLTTCRGLGLADI 300
      |||
DB      241 NLFGRSALTYASLTIKENLKTSGSEVGNVNFLLVTLALQAKAFLLTTCRGLGLADI 300
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QY 301 DYPIMNEHINKKEEFVNILPTLSNTPSNPYEKARGSDKAKIMEAKPGYALVGF 360  
DB 301 DYPIMNEHINKKEEFVNILPTLSNTPSNPYEKARGSDKAKIMEAKPGYALVGF 360  
QY 361 ISKDSIAVLKYQAKLKHNQIDKDSISEIYVGIDKLLCPDQSEQMYTNKLAFPNEY 420  
DB 361 ISKDSIAVLKYQAKLKHNQIDKDSISEIYVGIDKLLCPDQSEQMYTNKLAFPNEY 420  
QY 421 ITXIAFTKKNLSRYEVTANFYDSSTGIDLNKKKISSSEAFSMLNANDGYMPTGTT 480  
DB 421 ITXIAFTKKNLSRYEVTANFYDSSTGIDLNKKKISSSEAFSMLNANDGYMPTGTT 480  
QY 481 SETFLTPINGFGLVVDENSLVTLTCKSYLRETLATDLSNKTCLIVPNGFISINVEN 540  
DB 481 SETFLTPINGFGLVVDENSLVTLTCKSYLRETLATDLSNKTCLIVPNGFISINVEN 540  
QY 541 GNLEGENLEPWKANNKNAAYVDHTGAVNGTKVLYVHEDGFSQFIDGDKLKTEYVIQYIV 600  
DB 541 GNLEGENLEPWKANNKNAAYVDHTGAVNGTKVLYVHEDGFSQFIDGDKLKTEYVIQYIV 600  
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DB 601 KGRKAIYLDKRNKGDYIEETNNELDFQAVTRPTITGDSRVHLIFTSQNGEBAFGN 660  
QY 661 FIISIRPSEBELSPELIKSDAWVSGQTIWISGNSINSVNGTFRONLSLESYSTYS 720  
DB 661 FIISIRPSEBELSPELIKSDAWVSGQTIWISGNSINSVNGTFRONLSLESYSTYS 720  
QY 721 NFNVNGFGKVTIRNSREVVERSYLOFSSKYISEKFTTTNNGLVYELSRASSRGVIN 780  
DB 721 NFNVNGFGKVTIRNSREVVERSYLOFSSKYISEKFTTTNNGLVYELSRASSRGVIN 780  
QY 781 GDFSIX 786  
DB 781 GDFSIX 786

RESULT 2  
US-10-473-687-2  
Sequence 2, Application US/10473687  
Publication No. US2004013942A1  
GENERAL INFORMATION:  
APPLICANT: Miles, Paul  
APPLICANT: Kramer, Vance  
APPLICANT: Shen, Zhicheng  
APPLICANT: Shokkoski, Frank  
APPLICANT: Warren, Greg  
TITLE OF INVENTION: Novel Pesticidal Toxins  
FILE REFERENCE: S-60000PCT  
CURRENT APPLICATION NUMBER: US/10/473,687  
CURRENT FILING DATE: 2003-09-27  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 2  
LENGTH: 787  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis  
US-10-473-687-2

Query Match 87.8%; Score 3507.5; DB 4; Length 787;  
Best Local Similarity 87.3%; Pred. No. 9, 8e-207;  
Matches 687; Conservative 46; Mismatches 53; Indels 1; Gaps 1;  
QY 1 MOKNN-KLSVKALPSFIDYFNGIYGPATGIKDIMNIFFKNTGGDLTDEILKNOQLNE 59  
DB 1 MNKNNTKLNARALPSFIDYFNGIYGPATGIKDIMNIFKPDTCGNLTJDEILKNOQLNE 60  
QY 60 ISGKLDGVNGSLNDLLAOGNLDTELSKEIKLIANEONKVLNVTGLDAILNMLNTYLPK 119  
DB 61 ISGKLDGVNGSLNDLLAOGNLDTELSKEIKLIANEONQVLNVTGLDAILNMLNTYLPK 120  
QY 120 ITSMUSDWKNQYVALGLQIEYLSKQKEISDKLDVINNVVLNSTLTETPAVQRKYNV 179

DB 121 ITSMUSDWKNQYVALSLQIEYLSKQKEISDKLDVINNVVLNSTLTETPAVQRKYNV 180  
QY 180 EKFEALTSATEYNLTKYQDSSHTDIDBELTEITELAKSVTKQDVDFEFLYNTFHDVWG 239  
DB 181 EKFEALTSATEYNLTKYQDSSHTDIDBELTEITELAKSVTKQDVDFEFLYNTFHDVWG 240  
QY 240 NNLFGSALKTASELAKNLTSGSEGVNVPFLIVTALQAKAFLLTTCRKLGLAD 299  
DB 241 NNLFGSALKTASELAKNLTSGSEGVNVPFLIVTALQAKAFLLTTCRKLGLAD 300  
QY 300 IYTPIMNEHINKKEEFVNILPTLSNTPSNPYEKARGSDKAKIMEAKPGYALVGF 359  
DB 301 IYTPIMNEHINKKEEFVNILPTLSNTPSNPYEKARGSDKAKIMEAKPGYALVGF 360  
QY 360 EISKDSIAVLKYQAKLKHNQIDKDSISEIYVGIDKLLCPDQSEQMYTNKLAFPNEY 419  
DB 361 EMSNDSITVLKAYQAKLKODYQVDKDSISEIYVGMDKLLCPDQSEQIYYTNNAIFPNEY 420  
QY 420 VITKIAFTKKNLSRYEVTANFYDSSTGIDLNKKKISSSEAFSMLNANDGYMPTGTT 479  
DB 421 VITKIAFTKKNLSRYEVTANFYDSSTGIDLNKKKISSSEAFSMLNANDGYMPTGTT 480  
QY 480 ISETFLTPINGFGLVVDENSLVTLTCKSYLRETLATDLSNKTCLIVPNGFISINIVE 539  
DB 481 ISETFLTPINGFGLVVDENSLVTLTCKSYLRETLATDLSNKTCLIVPNGFISINIVE 540  
QY 540 NNLBGENLEPWKANNKNAAYVDHTGAVNGTKVLYVHEDGFSQFIDGDKLKTEYVIQYI 599  
DB 541 NNLBGENLEPWKANNKNAAYVDHTGAVNGTKVLYVHEDGFSQFIDGDKLKTEYVIQYI 600  
QY 600 VNGKAIYLDKRNKGDYIEETNNELDFQAVTRPTITGDSRVHLIFTSQNGEBAFGN 659  
DB 601 VNGKAIYLDKRNKGDYIEETNNELDFQAVTRPTITGDSRVHLIFTSQNGEBAFGN 660  
QY 660 NFIISEIRPSEBELSPELIKSDAWVSGQTIWISGNSINSVNGTFRONLSLESYSTYS 719  
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QY 720 MNFNNGFGKVTIRNSREVVERSYLOFSSKYISEKFTTTNNGLVYELSRASSRGVIN 779  
DB 721 MNFNNGFGKVTIRNSREVLFEKNYPOLSPEKFTTAANNGLVYELSRFTSGAIN 780  
QY 780 FDFSIX 786  
DB 781 FDFSIX 787

RESULT 3  
US-10-505-315-7  
Sequence 7, Application US/10505315  
Publication No. US20050210545A1  
GENERAL INFORMATION:  
APPLICANT: Syngenta Participations AG  
APPLICANT: Warren, Greg  
APPLICANT: Shokkoski, Frank  
APPLICANT: Kramer, Vance  
TITLE OF INVENTION: Novel Vip3 Toxins and Methods of Use  
FILE REFERENCE: 60163PCT  
CURRENT APPLICATION NUMBER: US/10/505,315  
CURRENT FILING DATE: 2004-08-19  
PRIOR APPLICATION NUMBER: US 60/362250  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 7  
LENGTH: 787  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (1)..(787)



OTHER INFORMATION: vip3b Toxin  
US-10-505-315-7

Query Match 87.8%; Score 3507.5; DB 5; Length 787;  
Best Local Similarity 87.3%; Pred. No. 9.8e-207;  
Matches 687; Conservative 46; Mismatches 53; Indels 1; Gaps 1;

QY 1 MORNN-KLSVYKALPSFIDYNGIYGFATGDKIDINMMI FKTNTGDDLTLDELTKNQOOLNE 59  
DB 1 MNKNNTKLNARALPSFIDYNGIYGFATGDKIDINMMI FKTDTGSNLTLDLTKNQOOLNE 60  
QY 60 ISGKLDGVNGLNDLDAQGLDTELSEKIIKIANEQKVANDVTKDAINMLNTYLPK 119  
DB 61 ISGKLDGVNGLNDLDAQGLDTELSEKIIKIANEQKVANDVTKDAINMLNTYLPK 120  
QY 120 ITSMGLDVNKNYALGLQIEYLSKQLEISDKLDVINVNVLINSTLEIPAYORIKYVN 179  
DB 121 ITSMGLDVNKNYALGLQIEYLSKQLEISDKLDVINVNVLINSTLEIPAYORIKYVN 180  
QY 180 EKFEALTSATEYMLKTKODSSHDDIDELTELTELAKSVTKNDVGEFYLNTFHDVMIG 239  
DB 181 EKFEALTSATEYMLKTKODSSHDDIDELTELTELAKSVTKNDVGEFYLNTFHDVMIG 240  
QY 240 NNIFGRSALKTASSELIAKENLKTSGSEVGNVNFLLVLTALQAKAFLLTTCRKLGLAD 239  
DB 241 NNIFGRSALKTASSELIAKENLKTSGSEVGNVNFLLVLTALQAKAFLLTTCRKLGLAD 300  
QY 300 IDYTPIMNHLNKEKEEFVNIILPTLSNTFSNPNYEKARSDSDAKIIMAKXGYALVGR 359  
DB 301 IDYTPIMNHLNKEKEEFVNIILPTLSNTFSNPNYEKARSDSDAKIIMAKXGYALVGR 360  
QY 360 ELSKSDIAVLKQVQAKLKHNQYQIDKQSLSEIYVGDIDKLCPPQSEOMYTTNKLAFPNEX 419  
DB 361 ELSKSDIAVLKQVQAKLKHNQYQIDKQSLSEIYVGDIDKLCPPQSEOMYTTNKLAFPNEX 420  
QY 420 VITTKLAFTKCLNSLRVEYTNANFYDSSGTGDIIDLNKKKIESSEAEFSMLNANDGVNMEIGT 479  
DB 421 VITTKLAFTKCLNSLRVEYTNANFYDSSGTGDIIDLNKKKIESSEAEFSMLNANDGVNMEIGT 480  
QY 480 ISFTFLTPINGFGLVVDENSLVLTTCYSYLRRETLATDLSNKEYKLIYPPNGFISNIYE 539  
DB 481 ISFTFLTPINGFGLVVDENSLVLTTCYSYLRRETLATDLSNKEYKLIYPPNGFISNIYE 540  
QY 540 NGNLEGENLEPMWANNKNAAYVDHTGVNGTKVLVYHDEGEFSQFIGDKLTKLXTEYVYOYI 599  
DB 541 NGNLEGENLEPMWANNKNAAYVDHTGVNGTKVLVYHDEGEFSQFIGDKLTKLXTEYVYOYI 600  
QY 600 VYKGAALYLDKDEKNGDIYEEITNNLEDFQAVTKRFLITGDSRVHLIFTSQNGEBAFG 659  
DB 601 VYKGAALYLDKDEKNGDIYEEITNNLEDFQAVTKRFLITGDSRVHLIFTSQNGEBAFG 660  
QY 660 NPLISIRSEBELLSPELLKSDAWGSGQVWISGNSLNTSNVNGTFRQNLSEBSYTS 719  
DB 661 NPLISIRSEBELLSPELLKSDAWGSGQVWISGNSLNTSNVNGTFRQNLSEBSYTS 720  
QY 720 MNPNVNGFGVKTIRNSREVVEERSYLOFSKYISEKRTTNTNNGLYVELSRASSGVIN 779  
DB 721 MNPNVNGFGVKTIRNSREVVEERSYLOFSKYISEKRTTNTNNGLYVELSRASSGVIN 780  
QY 780 FGDPSIK 786  
DB 781 PRNFSIX 787

RESULT 4  
US-10-452-002A-54

Sequence 54, Application US/10452002A  
Publication No. US20030236195A1  
GENERAL INFORMATION:  
APPLICANT: Jerald S. Felteelson  
APPLICANT: H. Ernest Schmept  
APPLICANT: Kenneth E. Narva  
APPLICANT: Brian A. Stockhoff

APPLICANT: James L. Schmeits  
APPLICANT: David Joewer  
APPLICANT: Charles J. Dullum  
APPLICANT: Judy Muller-Cohn  
APPLICANT: Lisa Stamp  
APPLICANT: George Morill  
APPLICANT: Stacey Finstad Lee  
TITLE OF INVENTION: No. US20030236195A1el Pesticidal Proteins and Methods of Using 1  
FILE REFERENCE: MA708C201  
CURRENT APPLICATION NUMBER: US/10/452, 002A  
CURRENT FILING DATE: 2003-05-30  
PRIOR APPLICATION NUMBER: 09/307,106  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: 09/073,898  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 08/960,780  
PRIOR FILING DATE: 1997-10-30  
PRIOR APPLICATION NUMBER: 60/029,848  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 54  
LENGTH: 787  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis strain KB59A4-6  
US-10-452-002A-54

Query Match 87.7%; Score 3505; DB 4; Length 787;  
Best Local Similarity 87.1%; Pred. No. 1.4e-206;  
Matches 682; Conservative 45; Mismatches 56; Indels 0; Gaps 0;

QY 4 NNKLSYKALPSFIDYNGIYGFATGDKIDINMMI FKTNTGDDLTLDELTKNQOOLNEISGK 63  
DB 5 NTKLNARALPSFIDYNGIYGFATGDKIDINMMI FKTDTGSNLTLDLTKNQOOLNEISGK 64  
QY 64 LDGVNGLNDLDAQGLDTELSEKIIKIANEQKVANDVTKDAINMLNTYLPK 123  
DB 65 LDGVNGLNDLDAQGLDTELSEKIIKIANEQKVANDVTKDAINMLNTYLPK 124  
QY 124 LSDVMKNYALGLQIEYLSKQLEISDKLDVINVNVLINSTLEIPAYORIKYVKEFE 183  
DB 125 LSDVMKNYALGLQIEYLSKQLEISDKLDVINVNVLINSTLEIPAYORIKYVKEFE 184  
QY 184 ALTSATEYMLKTKODSSHDDIDELTELTELAKSVTKNDVGEFYLNTFHDVMIGNLF 243  
DB 185 ELTPAETTLKVKQSSPADIDELTELTELAKSVTKNDVGEFYLNTFHDVMIGNLF 244  
QY 244 GRSALKTASSELIAKENLKTSGSEVGNVNFLLVLTALQAKAFLLTTCRKLGLADIDYT 303  
DB 245 GRSALKTASSELIAKENLKTSGSEVGNVNFLLVLTALQAKAFLLTTCRKLGLADIDYT 304  
QY 304 PIMNHLNKEKEEFVNIILPTLSNTFSNPNYEKARSDSDAKIIMAKXGYALVGRISK 363  
DB 305 SIMNHLNKEKEEFVNIILPTLSNTFSNPNYEKARSDSDAKIIMAKXGYALVGRISK 364  
QY 364 DSIYAVLKQVQAKLKHNQYQIDKQSLSEIYVGDIDKLCPPQSEOMYTTNKLAFPNEXYITK 423  
DB 365 DSIYAVLKQVQAKLKHNQYQIDKQSLSEIYVGDIDKLCPPQSEOMYTTNKLAFPNEXYITK 424  
QY 424 IAPTKCLNSLRVEYTNANFYDSSGTGDIIDLNKKKIESSEAEFSMLNANDGVNMEIGTISFT 483  
DB 425 IDFTKMKTKLRYEVTANSYDSSGTGDIIDLNKKKIESSEAEFSMLNANDGVNMEIGTISFT 484  
QY 484 FLTPINGFGLVVDENSLVLTTCYSYLRRETLATDLSNKEYKLIYPPNGFISNIYENGL 543  
DB 485 FLTPINGFGLVVDENSLVLTTCYSYLRRETLATDLSNKEYKLIYPPNGFISNIYENGL 544  
QY 544 EGENLEPMWANNKNAAYVDHTGVNGTKVLVYHDEGEFSQFIGDKLTKLXTEYVYOYIVK 603  
DB 545 EGENLEPMWANNKNAAYVDHTGVNGTKVLVYHDEGEFSQFIGDKLTKLXTEYVYOYIVK 604  
QY 604 AALYLDKDEKNGDIYEEITNNLEDFQAVTKRFLITGDSRVHLIFTSQNGEBAFGFNII 663  
DB 605 AALYLDKDEKNGDIYEEITNNLEDFQAVTKRFLITGDSRVHLIFTSQNGEBAFGFNII 664

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Db      605 ASITYLKDKKNENSIYEIINNDEEGFQVTKRPIITGDSGCIHLIFTSONGEGAFGNGFTII 664
Qy      664 SEIRSEELLSPDLIKSDAMVGSOGTWMISGNSLINSVNGTFRONLSIESYSTYSMNFN 723
      665 SEIRSEELLSPDLIKSDAMVGSOGTWMISGNSLINSVNGTFRONLPLESYSTYSMNFT 724
Qy      724 VNGFGKVTIRNSREVRPERSYIQFSSKTISEKFTTTTNNGTGLYVELSRASRGVINFGEF 783
      725 VNGFGKVTIRNSREVRPERSYIQFSSKTISEKFTTTTNNGTGLYVELSRASRGVINFGEF 784
Qy      784 SIK 786
      785 SIK 787

RESULT 5
US-10-698-096-25
; Sequence 25, Application US/10698096
; Publication No. US20040128716A1
; GENERAL INFORMATION:
; APPLICANT: Narva, Kenneth
; TITLE OF INVENTION: Polynucleotides, Pesticidal Proteins, and Novel Methods of Using
; FILE REFERENCE: MA-708CDCl
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 09/850,351
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 09/073,898
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 08/690,780
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,848
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-698-096-25

Query Match      87.7%; Score 3505; DB 4; Length 787;
Beet Local Similarity 87.1%; Pred. No. 1.4e-206;
Matches 682; Conservative 45; Mismatches 56; Indels 0; Gaps 0;

Qy      4 NNNKSVKALPSFIDYFNGIYGFATGIDIMNMIFFKTNNGDGLTDELILKNQOLNEISGK 63
      5 NTKLNARALPSFIDYFNGIYGFATGIDIMNMIFFKTNNGDGLTDELILKNQOLNEISGK 64
Qy      64 LDGVNGSLINDLLAOGNLDTELSEKILKIANEQNVLVNTKLDALINMLNTYLPKITSM 123
      65 LDGVNGSLINDLLAOGNLDTELSEKILKIANEQNVLVNTKLDALINMLNTYLPKITSM 124
Qy      124 LSDVKQNYVALGLQIEYLSKQIKESDKLDVINNVNLINSTLTETTPAYQRIKYVNEKFE 183
      125 LSDVKQNYVALSIQVEYLSKQIKESDKLDVINNVNLINSTLTETTPAYQRIKYVNEKFE 184
Qy      184 ALTSATETNNLKTQKQSSHTDILDELTELTELAKSYTKNDVDFEYVNTTFHDVWAGNULF 243
      185 ELTFETETTLTKVKQSSPADILDELTELTELAKSYTKNDVDFEYVNTTFHDVWAGNULF 244
Qy      244 GRSALKTASELLIAKENLKTSGSEVGNVNFLLVLTALQAKAFLLITTRKLLGLADIDYT 303
      245 GRSALKTASELLIAKENVKTSGSEVGNVNFLLVLTALQAKAFLLITTRKLLGLADIDYT 304
Qy      304 PYNNEHLNKEKEEPPRVNLLPILSNTPSNPNTYKAGSDKAKIIMEAKGYALVGFELISK 363
      305 SINNEHLNKEKEEPPRVNLLPILSNTPSNPNTYKAGSDKAKIIMEAKGYALVGFELISK 364
Qy      364 DSIAVLTKYQAKLKNYVQIDKDSLEIYQDIDKLLCPDQSEQMYTKIAFPNEYVYTK 423
      365 DSNITVLKYVEAKLKNYVQIDKDSLEIYQDIDKLLCPDQSEQMYTKIAFPNEYVYTK 424
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Qy      424 IAFYTKLNSIARYEVTANFYDSSGTGIDLNKKKIESSEAEFSMLNANNQGVNPIGTISRT 483
      425 IDFTKMKTLRYEVANSDSSGTGIDLNKKKIESSEAEFSMLNANNQGVNPIGTISRT 484
Qy      484 FLTPINGFGLVVDENSRVLTITCKSYLRETLATDLSNKEKYLYPPNPGISNIYENGUL 543
      485 FLTPINGFGLVVDENSRVLTITCKSYLRETLATDLSNKEKYLYPPNPGISNIYENGUL 544
Qy      544 EGENLEPMWANKKNAVYVHTGNGTKYLYVHEDDFSGFIDKLLKTKRYIYQYIVKCK 603
      545 EGENLEPMWANKKNAVYVHTGNGTKYLYVHEDDFSGFIDKLLKTKRYIYQYIVKCK 604
Qy      604 AAIYLKDEKNGDIYIETNNLEDFQAYTKRPIITGDSRGVHLIFTSONGEGAFGNGFTII 663
      605 ASITYLKDKKNENSIYEIINNDEEGFQVTKRPIITGDSGCIHLIFTSONGEGAFGNGFTII 664
Qy      664 SEIRSEELLSPDLIKSDAMVGSOGTWMISGNSLINSVNGTFRONLSIESYSTYSMNFN 723
      665 SEIRSEELLSPDLIKSDAMVGSOGTWMISGNSLINSVNGTFRONLPLESYSTYSMNFT 724
Qy      724 VNGFGKVTIRNSREVRPERSYIQFSSKTISEKFTTTTNNGTGLYVELSRASRGVINFGEF 783
      725 VNGFGKVTIRNSREVRPERSYIQFSSKTISEKFTTTTNNGTGLYVELSRASRGVINFGEF 784
Qy      784 SIK 786
      785 SIK 787
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RESULT 6
US-10-698-096-27
; Sequence 27, Application US/10698096
; Publication No. US20040128716A1
; GENERAL INFORMATION:
; APPLICANT: Narva, Kenneth
; TITLE OF INVENTION: Polynucleotides, Pesticidal Proteins, and Novel Methods of Using
; FILE REFERENCE: MA-708CDCl
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 09/850,351
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 09/073,898
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 08/690,780
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,848
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 788
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-698-096-27

Query Match      87.7%; Score 3505; DB 4; Length 788;
Beet Local Similarity 87.1%; Pred. No. 1.4e-206;
Matches 682; Conservative 45; Mismatches 56; Indels 0; Gaps 0;

Qy      4 NNNKSVKALPSFIDYFNGIYGFATGIDIMNMIFFKTNNGDGLTDELILKNQOLNEISGK 63
      6 NTKLNARALPSFIDYFNGIYGFATGIDIMNMIFFKTNNGDGLTDELILKNQOLNEISGK 65
Qy      64 LDGVNGSLINDLLAOGNLDTELSEKILKIANEQNVLVNTKLDALINMLNTYLPKITSM 123
      66 LDGVNGSLINDLLAOGNLDTELSEKILKIANEQNVLVNTKLDALINMLNTYLPKITSM 125
Qy      124 LSDVKQNYVALGLQIEYLSKQIKESDKLDVINNVNLINSTLTETTPAYQRIKYVNEKFE 183
      126 LSDVKQNYVALSIQVEYLSKQIKESDKLDVINNVNLINSTLTETTPAYQRIKYVNEKFE 185
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[illegible]

QY	783 FSIX	786
Db	785 VSIX	788

540 NGNLGEGNLEPMKANKNAVYVDHGTGVNGTKVLVYHEDGESFSDIIGDKLKLTKEVVIQYL 599

Db 541 NSGIEBNDLEPMKANKNAAYVDHTGVNGTKALVHKDGFSGFIDGDKLPKTEYVIQYT 600  
Qy 600 VKGKAAIYLKDEKNGDIYIEETNNLEDFQAVTKRFTTGTSSRVHLIFTSQGEARFG 659  
Db 601 VKGKPSIHLKDEMTGYIHYEDTNNNKDYOTITKRFITGTDLKGVIILKSQNGDEAMGD 660  
Qy 660 NFIISEIRPEEELISPELLIKSDAMVGSQGTWISGNSININSNVNGTFRQMLSLSESYTYS 719  
Db 661 KFTLLEIKPAEDLLSPBLINPNSWITTPGASISGNKLPINLGTNGTFRQSLINSYSTYS 720  
Qy 720 MNFNNGFGKVTIRNSREVEFERSYLOFSKYSISEKFTTTNTNGLYVELSRAS-SRGVI 778  
Db 721 ISFTASGPFVTVYRNSRGVLFERSNLMSSHISGTFKTESNNTGLYVELSRSGGGCHI 780  
Qy 779 NFGDPSIK 786  
Db 781 SFENVSIK 788

RESULT 10  
US-10-505-315-11  
; Sequence 11, Application US/10505315  
; Publication No. US20050210545A1  
; GENERAL INFORMATION:  
; APPLICANT: Syngenta Participations AG  
; APPLICANT: Shen, Zhicheng  
; APPLICANT: Warren, Gregory  
; APPLICANT: Shokoski, Frank  
; APPLICANT: Kramer, Vance  
; TITLE OF INVENTION: Novel Vip3 Toxins and Methods of Use  
; FILE REFERENCE: 60163PCT  
; CURRENT APPLICATION NUMBER: US/10/505,315  
; CURRENT FILING DATE: 2004-08-19  
; PRIOR APPLICATION NUMBER: US 60/362250  
; PRIOR FILING DATE: 2002-03-06  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patent version 3.2  
; SEQ ID NO 11  
; LENGTH: 788  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Hybrid Vip3A-C toxin  
US-10-505-315-11

Query Match 81.0%; Score 3235; DB 5; Length 788;  
Best Local Similarity 80.5%; Pred. No. 5.3e-190;  
Matches 634; Conservative 64; Mismatches 88; Indels 2; Gaps 2;

Qy 1 MOKNN-KLSVKALPSFIDYNGIYGFATGIKOIMNMIKTNNGDGLTDLDELKNOQLNE 59  
Db 1 MOKNNKTLSTRALPSFIDYNGIYGFATGIKOIMNMIKTDGDLTDLDELKNOQLNE 60  
Qy 60 ISGKLDGVNGSLNDLLAOGNLTDELSEKILKIANEQNKVLDVNTKLDALINMLNTYLPK 119  
Db 61 ISGKLDGVNGSLNDLLAOGNLTDELSEKILKIANEQNKVLDVNTKLDALINMLNTYLPK 120  
Qy 120 ITSMUSDVKNONVALGLOIEYLSKQIKESIDKLDVINNVNLINSTLTETPAYORIKYVN 179  
Db 121 ITSMUSDVKNONVALGLOIEYLSKQIKESIDKLDVINNVNLINSTLTETPAYORIKYVN 180  
Qy 180 EKPEALTSATETMLKTODSSHDTLIDELTELTELAKSVTKNDVGDPEPLNTFHVVMG 239  
Db 181 EKPEELTFPTEISSKVKKQSPADLIDELTELTELAKSVTKNDVGDPEPLNTFHVVMG 240  
Qy 240 NNLFGRSALKTASELITAKENLKTSGSEGVGVNPLVLTPALQAKAFELTTCRKLGLAD 299  
Db 241 NNLFGRSALKTASELITAKENLKTSGSEGVGVNPLVLTPALQAKAFELTTCRKLGLAD 300  
Qy 300 IDYTPIMNHLNKEKEEPRVNIPTLSNTPSNPNYERKAGSDYQAKIMEAKGVYLVGF 359  
Db 301 IDYTSIMNHLNKEKEEPRVNIPTLSNTPSNPNYERKAGSDYQAKIMEAKGVYLVGF 360

Qy 360 EISKDSIALVLYQVQAKLKHNQYQIDKDSLSIEYVGDIDKLLCPDQSEGMYYTINKIAPENEX 419  
Db 361 EISNDSITVLKVEEAKLKQNYQYDQKSLSEVYIGDMDKLLCPDQSEGIYTTNNIVFPNEX 420  
Qy 420 VITKIAFTKQNSLRREYVNAFDDSSGTGDIIDLKKKIESSEAFSMLNANDGVNPIGT 479  
Db 421 VITKIDFTKMKKILRYEVANFDDSSGTGEIDLKKKVESEAEYRTLISANDGVNPLGV 480  
Qy 480 ISFTPLTPINGFGVVDENSRVLTLCKSYLREFTLATDLSNKTETKLIYPNGFISNIVE 539  
Db 481 ISFTPLTPINGFGVQADENSRVLTLCKSYLREFTLATDLSNKTETKLIYPNGFISNIVE 540  
Qy 540 NGNLEBENLEPMKANKNAAYVDHTGVNGTKALVYHEDGFSGFIDGDKLPKTEYVIQYT 599  
Db 541 NSGIEBNDLEPMKANKNAAYVDHTGVNGTKALVYHEDGSIQFIDGDKLPKTEYVIQYT 600  
Qy 600 VKGKAAIYLKDEKNGDIYIEETNNLEDFQAVTKRFTTGTSSRVHLIFTSQGEARFG 659  
Db 601 VKGKPSIHLKDEMTGYIHYEDTNNNKDYOTITKRFITGTDLKGVIILKSQNGDEAMGD 660  
Qy 660 NFIISEIRPEEELISPELLIKSDAMVGSQGTWISGNSININSNVNGTFRQMLSLSESYTYS 719  
Db 661 KFTLLEIKPAEDLLSPBLINPNSWITTPGASISGNKLPINLGTNGTFRQSLINSYSTYS 720  
Qy 720 MNFNNGFGKVTIRNSREVEFERSYLOFSKYSISEKFTTTNTNGLYVELSRAS-SRGVI 778  
Db 721 ISFTASGPFVTVYRNSRGVLFERSNLMSSHISGTFKTESNNTGLYVELSRSGGGCHI 780  
Qy 779 NFGDPSIK 786  
Db 781 SFENVSIK 788

RESULT 11  
US-10-099-285-82  
; Sequence 82, Application US/10099285  
; Publication No. US20030105319A1  
; GENERAL INFORMATION:  
; APPLICANT: Schneck, H. Ernest  
; Wicker, Carol  
; Narva, Kenneth E.  
; Walz, Michelle  
; Stockhoff, Brian  
; Muller-Cohn, Judy  
; TITLE OF INVENTION: Toxins Active Against Peets  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanichik, Lloyd & Saliwanichik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/099,285  
; FILING DATE: 15-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/002,285  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/886,615  
; FILING DATE: 1-JUL-1997  
; APPLICATION NUMBER: US 08/674,002  
; FILING DATE: 1-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sanders, Jay M.  
; REGISTRATION NUMBER: 39,355  
; REFERENCE/DOCKET NUMBER: MA-701C2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 82:  
US-10-099-285-82

Query Match 79.7%; Score 3182.5; DB 4; Length 789;  
Best Local Similarity 79.0%; Pred. No. 8,8e-187;  
Matches 624; Conservative 69; Mismatches 92; Indels 5; Gaps 3;  
QY 1 MOKNN-KLSVKAALPSIDYFNGIYGFATGIKDIMNMIKFTNTGGDLTLDLILKNOQOLNE 59  
DB 1 MNKNNTKLSRALPSFIDYFNGIYGFATGIKDIMNMIKFTNTGGDLTLDLILKNOQOLNE 60  
QY 60 ISGKLDGVNGSLNDLIAQGNLDTLSKEILKIANEQNKVNDVNTKLDAINMTMTYLPK 119  
DB 61 ISGKLDGVNGSLNDLIAQGNLDTLSKEILKIANEQNKVNDVNTKLDAINMTMTYLPK 120  
QY 120 ITSMUSDVWKQNYVALGQIEYLSKQLEISDKLDIVNVNVLINSTLTETTPAYQRIKYN 179  
DB 121 ITSMUSDVWKQNYVALGQIEYLSKQLEISDKLDIVNVNVLINSTLTETTPAYQRIKYN 180  
QY 180 EKFEALTSATETNLTQDSSHTDILDELTELAKSVTKNDVDGFEFYLTTFHDVMIG 239  
DB 181 EKFEALTSATETNLTQDSSHTDILDELTELAKSVTKNDVDGFEFYLTTFHDVMIG 240  
QY 240 NNLFGRSALKTASELAKENLTSGSEVGNVNVNVLVLTALQAKAFITTTCKLIGLAD 299  
DB 241 NNLFGRSALKTASELAKENLTSGSEVGNVNVNVLVLTALQAKAFITTTCKLIGLAD 300  
QY 300 IDYTPIMNEHLNKEKEEFPVNLPTLSNTPSNPTEKAGSDKAKIIMEAKRYALVGF 359  
DB 301 IDYTPIMNEHLNKEKEEFPVNLPTLSNTPSNPTEKAGSDKAKIIMEAKRYALVGF 360  
QY 360 EISKSIYLVKQYQAKLKHNYOIDQDSLEIYVGDIDKLCPDQSEQMYTNTKIAFPNEY 419  
DB 361 EMSNDSITVLKQYEAKLKQNYQVDQDSLEIYVGDIDKLCPDQSEQMYTNTKIAFPNEY 420  
QY 420 VITTKIAFTKQNSLAEYLTANFYDSSGTDIDLNKKIISSEAEBSMLAANDGVYMPYGT 479  
DB 421 VITTKIAFTKQNSLAEYLTANFYDSSGTDIDLNKKIISSEAEBSMLAANDGVYMPYGT 480  
QY 480 ISETFLPFPNGFGLVVDENSRLVTLTCKSYLRETLATDLSNKEFKLIVPPNGFISNIVE 539  
DB 481 ISETFLPFPNGFGLVVDENSRLVTLTCKSYLRETLATDLSNKEFKLIVPPNGFISNIVE 540  
QY 540 NGNLEGNELEPWKANKNAAYVDHTGVNGTVLVYHEDGEFSQFIDGDKLKTBEVYIOYI 599  
DB 541 NGNLEGNELEPWKANKNAAYVDHTGVNGTVLVYHEDGEFSQFIDGDKLKTBEVYIOYI 600  
QY 600 VKGAATYIKDEKNGDYIEETNNELEPQAVTRKFTIGTSSKRVHLIFTSQNGEBAFG 659  
DB 601 VKGAATYIKDEKNGDYIEETNNELEPQAVTRKFTIGTSSKRVHLIFTSQNGEBAFG 660  
QY 660 NFIIISIRPSEELSPILIKSDAWVSGQTIWISGSLININSNVNGTTPRONLSLSYSYYS 719  
DB 661 NFIIISIRPSEELSPILIKSDAWVSGQTIWISGSLININSNVNGTTPRONLSLSYSYYS 720  
QY 720 MNFVNVNGPKATYINNSREVVAFERSYLOPSSKYSIEKFTTTNTNGLYVELSPRASS--RG 776  
DB 721 VYFVSVDGANVRINSREVLFEKRYMS-GAKDVSEMFTEKPKONFYIELSGNNLVGGP 779  
QY 777 VINFGDPSIK 786  
DB 780 IVHFNVDYSIK 789

RESULT 12  
US-10-099-285-84  
Sequence 84, Application US/10099285  
Publication No. US20030105319A1  
GENERAL INFORMATION:  
APPLICANT: Schnepf, H. Ernest  
Wicker, Carol  
Narva, Kenneth E.  
Walz, Michelle  
Stockhoff, Brian  
Muller-Cohn, Judy  
TITLE OF INVENTION: Toxins Active Against Pests  
NUMBER OF SEQUENCES: 105  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/099,285  
FILING DATE: 15-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/002,285  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/886,615  
FILING DATE: 1-JUL-1997  
APPLICATION NUMBER: US 08/674,002  
FILING DATE: 1-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-701C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 84:  
US-10-099-285-84  
Query Match 79.6%; Score 3180.5; DB 4; Length 789;  
Best Local Similarity 78.9%; Pred. No. 1.2e-186;  
Matches 623; Conservative 70; Mismatches 92; Indels 5; Gaps 3;  
QY 1 MOKNN-KLSVKAALPSFIDYFNGIYGFATGIKDIMNMIKFTNTGGDLTLDLILKNOQOLNE 59  
DB 1 MNKNNTKLSRALPSFIDYFNGIYGFATGIKDIMNMIKFTNTGGDLTLDLILKNOQOLNE 60  
QY 60 ISGKLDGVNGSLNDLIAQGNLDTLSKEILKIANEQNKVNDVNTKLDAINMTMTYLPK 119  
DB 61 ISGKLDGVNGSLNDLIAQGNLDTLSKEILKIANEQNKVNDVNTKLDAINMTMTYLPK 120  
QY 120 ITSMUSDVWKQNYVALGQIEYLSKQLEISDKLDIVNVNVLINSTLTETTPAYQRIKYN 179  
DB 121 ITSMUSDVWKQNYVALGQIEYLSKQLEISDKLDIVNVNVLINSTLTETTPAYQRIKYN 180  
QY 180 EKFEALTSATETNLTQDSSHTDILDELTELAKSVTKNDVDGFEFYLTTFHDVMIG 239  
DB 181 EKFEALTSATETNLTQDSSHTDILDELTELAKSVTKNDVDGFEFYLTTFHDVMIG 240

[illegible]

Query	Match	79.5%	Score 3176.5	DB 4	Length 789
Best Local Similarity	78.9%	Pred. No. 2,1e-186			
Matches 623	Conservative 69	Mismatches 93	Indels 5	Gaps 3	
1	MOKANN-KLSYVALPSEFIDYFNGIYGAFANGIDINMMI.FKNTYGGDLTLDEILKNOQLNE	59			
1	MKNKNTLSARALPSFIDYFNGIYGAFANGIDINMMI.FKNTYGGDLTLDEILKNOQLNE	60			
60	ISGKLDGVNGLNDLLAQGNLDPTELSEKILKIANEQKVNLDVNTKLDALIMLMTYLPK	119			
61	ISGKLDGVNGLNDLLAQGNLDPTELSEKILKIANEQKVNLDVNTKLDALIMLMTYLPK	120			
120	ITSLSDVMKONVALGLOIELYSKOLKEISPKLVINWVNLINSTLEITPARYORIKVN	179			
121	ITSLSDVMKONVALSLOIELYSKOLKEISPKLVINWVNLINSTLEITPARYORIKVN	180			
180	EKPEALTSATETNLKTKQDSSTHTLDELTELTELAKSVTKNDVGEFEYLNTRFDVWIG	239			
181	EKPEALTPATETTLTKVKKQSSPADILDELTELTELAKSVTKNDVGEFEYLNTRFDVWIG	240			
240	NNLFGRSALKTASLLIAKENLTKSGSEVGNVYNFLVLTALQAAPFLTLTCRKLGLAD	299			
241	NNLFGRSALKTASLLIAKENLTKSGSEVGNVYNFLVLTALQAAPFLTLTCRKLGLAD	300			
300	IDYPIINNEHLNKKKEEFRVNIPLTLNTPSNPYEKARSGSDKAKIIMEAKPGYALVGF	359			
301	IDYTSIMNEHLNKKKEEFRVNIPLTLNTPSNPYEKARSGSDKAKIIMEAKPGYALVGF	360			
360	EISKDSIAVLKYQAULKHANYQIDKDSLSEIIVGDIIDLKCPDQSEQMYTNNKIAPNEX	419			
361	EMSNDSTIVLKVEEAKIKONYQVDKDSLSEIIVGDIIDLKCPDQSEQMYTNNKIAPNEX	420			
420	VITTIATFKKLNSLRVEVTANFDYSSNGDIDLNKKKIESSSEABFSMLNANNDDGYMPLGT	479			
421	VITTIATFKKLNSLRVEVTANFDYSSNGDIDLNKKKIESSSEABFSMLNANNDDGYMPLGT	480			
480	ISBETFLPPIINGFGLVDENSRLVTLTKCKSYLRETLATDLSENKETKLIIVPENGPIISNIVE	539			
481	ISBETFLPPIINGFGLVDENSRLVTLTKCKSYLRETLATDLSENKETKLIIVPENGPIISNIVE	540			
540	NGNLEGENLEBPYKANNKQAYVDHRTGNGVNTKVLVYHEDGESQPIIDKRLKATERYVIOYI	599			
541	NGNLEGENLEBPYKANNKQAYVDHRTGNGVNTKVLVYHEDGESQPIIDKRLKATERYVIOYI	600			
600	VKGKAAIYLVLEKDKGDIYEEITNNLEEDPOAVTKRFTITGDSASVHLIFTSONGEBAFGG	659			
601	VKGKPSIHLADENGYIHYEDTNNNLMDYOYITRFTITGDIKAGVYLILSKQNDDEAMGD	660			
660	NFIISIRPSBELISPELISKDAVWGSQGTWISGNSLINSNVNGTRONLSLESYTYS	719			
661	NFIILIESPSBKLSPELISPELISNVNTSGSTHISGNTLITLVQGGGKILKONVQIDSPSTYR	720			

Query 720 MNFNVNGFKVTIIRNSREVPERSYLOFSSKYISEKFTTTTNTNGLYVELSRASS---RG 776  
Db 721 VYFVSVDGANVRIIRNSREVLFEKRYMS-GAKOVSEMTTTFEKNFYIELSGNNLYGCP 779  
Query 777 VINFQDPSIK 786  
Db 780 IVHFYDVSIR 789

RESULT 14  
US-10-473-687-5  
; Sequence 5, Application US/10473687  
; Publication No. US20040133942A1  
; GENERAL INFORMATION:  
; APPLICANT: Kramer, Paul  
; APPLICANT: Miles, Paul  
; APPLICANT: Shen, Zhicheng  
; APPLICANT: Shokoski, Frank  
; APPLICANT: Warren, Greg  
; TITLE OF INVENTION: Novel Pesticidal Toxins  
; FILE REFERENCE: S-6000PCT  
; CURRENT APPLICATION NUMBER: US/10/473,687  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 5  
; LENGTH: 789  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-473-687-5

Query Match 79.5%; Score 3175.5; DB 4; Length 789;  
Beat Local Similarity 78.6%; Pred. No. 2.4e-186;  
Matches 621; Conservative 70; Mismatches 94; Indels 5; Gaps 3;

Query 1 MOKNN-KLSVKALPSFIDYENGIGYGFATGIDIMNMIFKNTGDLTLDEILKNOQLNE 59  
Db 1 MNKNNTKLSRALPSFIDYENGIGYGFATGIDIMNMIFKNTGDLTLDEILKNOQLNE 60  
Query 60 ISGKLDGVNGSLNDLIAQCNLTDELTELAKSVTNDVDGFEFYANTPHDVMWG 119  
Db 61 ISGKLDGVNGSLNDLIAQCNLTDELTELAKSVTNDVDGFEFYANTPHDVMWG 120  
Query 120 ITSMUSDVMKONYALGLQIEYLSKQLEISDKLDVINNVVINSTLTETTPAYORIKYVN 179  
Db 121 ITSMUSDVMKONYALGLQIEYLSKQLEISDKLDVINNVVINSTLTETTPAYORIKYVN 180  
Query 180 EKFEALTSATETNLTAKODSSHTDILDELTELTELAKSVTNDVDGFEFYANTPHDVMWG 239  
Db 181 EKFEALTSATETNLTAKODSSHTDILDELTELTELAKSVTNDVDGFEFYANTPHDVMWG 240  
Query 240 NNLFRSALKTASLILAKENLKTSGSEGVGVNFIIVLTALQAKAFLLTTCRKLGLAD 299  
Db 241 NNLFRSALKTASLILAKENLKTSGSEGVGVNFIIVLTALQAKAFLLTTCRKLGLAD 300  
Query 300 IDYTPIMNHELNKEKEEFRRVNIPLTSLNTFSNPYEKARGSDKAKIIMEAKPGYALVGF 359  
Db 301 IDYTPIMNHELNKEKEEFRRVNIPLTSLNTFSNPYEKARGSDKAKIIMEAKPGYALVGF 360  
Query 360 EISKDSIAVLKYQAKLGHNTQIDKDSISEIYGGIDKLCPCDQSEQIYYTNNIYFPEY 419  
Db 361 EISKDSIAVLKYQAKLGHNTQIDKDSISEIYGGIDKLCPCDQSEQIYYTNNIYFPEY 420  
Query 420 VITTKAFKKLNSLRYETANFYDSSGTDIDLNKKIISSEAEBSMLNANDGVYMPYGT 479  
Db 421 VITTKAFKKLNSLRYETANFYDSSGTDIDLNKKIISSEAEBSMLNANDGVYMPYGT 480  
Query 480 ISEFELPINSFGIYVDENSRLVTLTCSYLRRETLATDLSENKETKLVPNGFISNIVE 539  
Db 481 ISEFELPINSFGIYVDENSRLVTLTCSYLRRETLATDLSENKETKLVPNGFISNIVE 540  
Query 540 NGNLEGENLEPFWKANNKNAVVDHTGGVNGTKVLYVHEDGEFSQPIGDKLKLTEYVIOYI 599

Db 541 NSIEEDNLPEPKANNKNAVVDHTGGVNGTKVLYVHEDGEFSQPIGDKLKLTEYVIOYI 600  
Query 600 VYKGAIIYKDERKNGDIYEETNNELEDFQAVTKRPTGTDSRVHLFTSQNGERAFGC 659  
Db 601 VYKGSIIHLKDERNTGVIIHEDTNNNLEDYQYINKPFTTGTDLKGVLYLSQNGDEAWCD 660  
Query 660 NFILSEIRPSEELISPELISKDAWYSGOGTWISGNSINSVNGFRONLSLESYSTYS 719  
Db 661 NFILSEIRPSEELISPELISPELISKDAWYSGOGTWISGNSINSVNGFRONLSLESYSTYS 720  
Query 720 MNFNVNGFKVTIIRNSREVPERSYLOFSSKYISEKFTTTTNTNGLYVELSRASS---RG 776  
Db 721 VYFVSVDGANVRIIRNSREVLFEKRYMS-GAKOVSEMTTTFEKNFYIELSGNNLYGCP 779  
Query 777 VINFQDPSIK 786  
Db 780 IVHFYDVSIR 789

RESULT 15  
US-10-505-315-5  
; Sequence 5, Application US/10505315  
; Publication No. US20050210545A1  
; GENERAL INFORMATION:  
; APPLICANT: Syngenta Participations AG  
; APPLICANT: Shen, Zhicheng  
; APPLICANT: Warren, Gregory  
; APPLICANT: Shokoski, Frank  
; APPLICANT: Kramer, Vance  
; TITLE OF INVENTION: Novel Vip3 Toxins and Methods of Use  
; FILE REFERENCE: 60163PCT  
; CURRENT APPLICATION NUMBER: US/10/505,315  
; PRIOR FILING DATE: 2004-08-19  
; PRIOR APPLICATION NUMBER: US 60/362250  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 5  
; LENGTH: 789  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1) - (789)  
; OTHER INFORMATION: Vip3a toxin  
US-10-505-315-5

Query Match 79.5%; Score 3175.5; DB 5; Length 789;

Beat Local Similarity 78.6%; Pred. No. 2.4e-186;  
Matches 621; Conservative 70; Mismatches 94; Indels 5; Gaps 3;

Query 1 MOKNN-KLSVKALPSFIDYENGIGYGFATGIDIMNMIFKNTGDLTLDEILKNOQLNE 59  
Db 1 MNKNNTKLSRALPSFIDYENGIGYGFATGIDIMNMIFKNTGDLTLDEILKNOQLNE 60  
Query 60 ISGKLDGVNGSLNDLIAQCNLTDELTELAKSVTNDVDGFEFYANTPHDVMWG 119  
Db 61 ISGKLDGVNGSLNDLIAQCNLTDELTELAKSVTNDVDGFEFYANTPHDVMWG 120  
Query 120 ITSMUSDVMKONYALGLQIEYLSKQLEISDKLDVINNVVINSTLTETTPAYORIKYVN 179  
Db 121 ITSMUSDVMKONYALGLQIEYLSKQLEISDKLDVINNVVINSTLTETTPAYORIKYVN 180  
Query 180 EKFEALTSATETNLTAKODSSHTDILDELTELTELAKSVTNDVDGFEFYANTPHDVMWG 239  
Db 181 EKFEALTSATETNLTAKODSSHTDILDELTELTELAKSVTNDVDGFEFYANTPHDVMWG 240  
Query 240 NNLFRSALKTASLILAKENLKTSGSEGVGVNFIIVLTALQAKAFLLTTCRKLGLAD 299  
Db 241 NNLFRSALKTASLILAKENLKTSGSEGVGVNFIIVLTALQAKAFLLTTCRKLGLAD 300  
Query 300 IDYTPIMNHELNKEKEEFRRVNIPLTSLNTFSNPYEKARGSDKAKIIMEAKPGYALVGF 359



Db 301 IDYTSINNEHLNKEKEEFVNIILPTLSNTFSNPNYAKVKSDEDAKMIIVAKPGHALIGF 360  
Qy 360 EISKDSIAVAKVYQAKLNHNYQIDKDSLSIYVGDIDKLCPODSBOMYTNKIAFPNEY 419  
Db 361 EISNDSITVAKVEAKLKONYQVDDKDSLSEVIYGDMDKLCPODSEQIYYTNNIVFPNEY 420  
Qy 420 VITKIAFTKILNSLRVEVTANFYDSTGDIIDLNCKKIESSEAEFSMLNANDGVYMPIGT 479  
Db 421 VITKIDFTKGMKTLIRYEV TANFYDSTGEIDLNCKKVESSEAEYRTLSANDGVYMPILGV 480  
Qy 480 ISETFLTPINGFGLVVDENSRVLTLTCKSYLRETLATDLSNKETKLIIPPNGFISNIVE 539  
Db 481 ISETFLTPINGFGLVVDENSRVLTLTCKSYLRETLATDLSNKETKLIIPPNGFISNIVE 540  
Qy 540 NGULEGENTLEPMKANNKNAAYVDHTGNGVGTKVLVYHEDGESQPIGDKLKLTREYVIOYI 599  
Db 541 NGSIEEDNLEPMKANNKNAAYVDHTGNGVGTKVLVYHEDGESQPIGDKLKLTREYVIOYI 600  
Qy 600 VKGKAAYLKDCKNGDYIYEETNNLEDFQAVTKRPIGTGDSRVHLIFTSONGEBAFG 659  
Db 601 VKGKPSIHLKDENTGYIHYEDTNNLEDFQAVTKRPIGTGDLKGVYIILKSQNGDEAMGD 660  
Qy 660 NFIISEIRPSEELLSPELIKSDAMVGSQGTWISGNSLINSNVNGTFROMLSLESYSTS 719  
Db 661 NFIISEIRPSEELLSPELIKSDAMVGSQGTWISGNSLINSNVNGTFROMLSLESYSTS 720  
Qy 720 MNNVNGFGKVTIRNSREVPERSYLOFSKYSIEKFTTTNTNGLYVELSRASS--RG 776  
Db 721 VYFSVSGDANVRIRNSREVLFEKRYMS-GAKDVSEMPFTYKEKONFYIELSOGNNLYGCP 779  
Qy 777 VINFGDFSIR 786  
Db 780 IVHFPYDVSIK 789

Search completed: May 15, 2006, 20:47:49  
Job time : 171 secs

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QY	211	-LTEL- -KSVTKNDVDGEEFY-----LTFPHDVMIGNNLFGRSALKT	251
Db	246	VINQAAQGVSTIKNANNGENLEPAKQOASQSLGSLDNLINNAKQVTDIDINGAHTVDEA	305
QY	252	SELIAKENKTSGSSEGVNVNPLIVLTALQ-----KAPFLITL-----	290
Db	306	NGI--KQNGQNTMTANGIKQALADDAATGATVTFDADQAKQAVTATVNAENITSA	366
QY	291	-----CRKLGLADIIDY-----TPIMN- EHLN-----	311
Db	364	NGGNATQAEVEQAIKQVNAKQALNGVNAVQAHKDEATALINSNDLINOAKQALQOVQ	423
QY	312	-----KEKEEFRVNILLPTLSNTSPNPEYKARGS-----DKD-----AK	343
Db	424	NATTVAGVNNVKTQAOELNANMTQKQGLADKEQITADGFGFNADPDKQNAVNOAVAKAE	483
QY	346	IMEAKPGYALVGFELISKDSIAVLKYQOAKKHNYQIDKQSLSEIYVGDIIDKLCPQSE	405
Db	484	ALISATPDVVVTPSEI---TAALNKVTQAKNDLNGMTNLATATQONQHAIDQLEPNLNOAQ	540
QY	406	QWYTNKIA-----FPEHYVITKIAFTKK-----LNSLREYVTAIFYDSSTDGIDL	451
Db	541	RDEYSKQITQATLVPVNVNAIQQAATTLNDAMTQKQGIANKQAIKXSENYHDAADTKQTA	600
QY	452	NKKKIESSAEFSMILNANDGVYMPICITISEFLPPINGGLVVDENSRLVTLTCKSYLR	511
Db	601	YMNATYKAE---ELKQTTNPTMDP--NTIQQA-LTVYNDTNQALNGQKKA--DAKQDAK	653
QY	512	ETLLATLDSNKETKLIV-----PENGFLSNIVENGNGENLEBWKANKKNAVYDHTG	564
Db	654	TTLGTLHLNDQKQKQLTTQVEQAPDIATVNVNKHQ---AQULNNAMTNLNNAADQKTE	709
QY	565	GYN-----GTKLYV-----HEGBESQIFGDKL-KLKTBEYVIQIYKGAALYKLD	610
Db	710	TLNSINFTDADQAKDQADYNAVNAVSHAGILISKANGSNASTREYEQAMQVNEAKQALNGND	769
QY	611	-----EKQGDVYYEFTN--NELEDFQAVT	632
Db	770	NVQRAKDAKAKQVITNANDLNQAMTQKQGLADKQCTKANGFNPAADTKONAVNVNAHA	829
QY	633	KREFTGDBSSRVHLIFTSQ-----NGEENAF-----GGEFISBI-----PSPBE	671
Db	830	EQIISGTEPANVDPQOVAAQALQOVNAQKAGDLNGNHNLIQVAKONANATIDQLPPLNGPQKT	889
QY	672	LISPELISDANVWSQGTWISGNSLINTNSNNAVGTFRQNLSLBSYSTYSNMF	722
Db	890	ALKQDVSHAEIVTGVNAIKQNDALN---NAMGTLLKQOIQANSQVPSVDVF	937

[illegible]

Qy 678 IKSAMVGSQ-----GTWISGNSLN-----INSN--VNGFRONLSIESYSTY 718  
Db 1509 IAEIDINVEKMDINTITGKYVDNNTDKSIDFISISLVKQVKNGLVINSVSYSLDF 1568  
Qy 719 SMN-----FNVVGFVGNITRNSREVVEFSYLOPSSKYSSEKFTTTNTNG-YYELSGAS 773  
Db 1569 VKNSDGHNTSNFNMFLDN--ISFMWLFEPENINFDIKYFTLVGKTNLGYVEFICDN 1625  
Qy 774 SRGV-INFGDP 783  
Db 1626 NKONIDYFGEW 1636

RESULT 3  
US-11-087-099-12160  
; Sequence 12160, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450) B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 12160  
; LENGTH: 1778  
; TYPE: PRT  
; ORGANISM: *Listeria monocytogenes* EGD-e  
US-11-087-099-12160

Query Match 4.4%; Score 175; DB 11; Length 1778;  
Best Local Similarity 20.2%; Pred. No. 0.069;  
Matches 190; Conservative 140; Mismatches 314; Indels 298; Gaps 50;

Qy 4 NNTLS-VKALPSF--IDYFGIYRATGIDIMNMKTGTGDLT---LDELTKNQOL 56  
Db 487 SNRISDVSTLTJNPEPSLYIN-----ISNNVIR--TVGKMTLPSIKFYAQNNS 533  
Qy 57 LNEIS-----GKLDGVNGSLNDLLAQNLDTELSEKI-----LKIA 92  
Db 534 ISDISMHDMPNLRKVDSNNLTINIGTFDNLPGQLSDVHSNRITTSYVHDLPSLETF 593  
Qy 93 NEONKVLNDVNT---KLDALNIMLNTY-----LPKI-TSMLSDVKNQVYALG--- 135  
Db 594 NAQTNLTINIGTMDNLPDLTYVNLSPRIPSLAPIGDLPNLETLIVSDNNSYLRSGTMD 653  
Qy 136 -----IQIEYLS-----KOLKEISDGLDVANNVNLNSTITET--PATQIRKYN 179  
Db 654 GVEPLRILDLQNNYLANLTGTEGNSSISDLTNTLMTLRNNVYIDDISGLSTRLYYN 713  
Qy 180 -----EKFPALTSATETNLKTODSHTDI--LDELTELTELAKSVTKNDVGFERYLN 231  
Db 714 LDSNKEIDISALSNLTNLOELTEBNNKINISALSLENLKNLY--VSKNKI----- 763  
Qy 232 TFDVNIIGNNLFGRSALKTASE-----LIAKENLXTSGSEVGNVY 271  
Db 764 --IDISPVANMVRGALVTASNGTYTLPTVLSYQSSFTINPVIWYGTLLAASSIGNSG 821  
Qy 272 NF---LIVLTALQAKAPLITTCRKLIGLADIDYTPIMNEHLNKEEFVNILPTISNT 338  
Db 822 NYDQKITWTNMTATSSSTLF-----NFRRLKQGL-----TFSGT 856  
Qy 329 FSNPNTEKARGSKDKAKIIMEAKRGVALVGFESISKDSIAVLKYQAKLKH----- 378  
Db 857 VTQP-YKSA-----AKVTADAEQYTL-IDDTISBEQF--LKQVNAASSSGAPVTSDFAT 906  
Qy 379 -----NYQIDKDISISLIVGDIDK-----LPCPDQSBQWYTNKIAFPNRYV 420  
Db 907 VVDLNTFGEYEVTLTSEKDGIGQDSCKVIKVLHGAFAVISADQT-----ISYDQAT 958  
Qy 421 ITKIAFTKKLNS---LRBYTANFYDSSTGDIPLANKKISSSEAPSMLANNDGYMPT 477  
Db 959 IIEKQFLBEDIHASTDLDTALTITNF---STA-VNLNK-----GGDYVALNSENEDGVK--- 1007

Qy 478 GTISETFLTPNGFGLVVDENSRVLTLCKSYLRETLATDPLNSKETKLIYPMGPI SNI 537  
Db 1008 ---AEIYYVYT-----VAKDPAPITIS-----AKITITTDKSKTEA-----AFLDI 1048  
Qy 538 ---VENGNLSEGNLEPMKANNKAAVYDHT-----GGVNGT-KVLVYHDEGFESQFIG 585  
Db 1049 DADTNDGSIYTSNFA--TAVNLDRAGDYTVTLNATNEDGVKATPVEVIVHQQGERPVITAD 1216  
Qy 586 DKL-KLKEVYIQ--IVKGKAAIYLDKKNKGYIYEETNNELE-DQAVTKRFTITGDS 641  
Db 1101 -KATISTNTAQQYKAKKINETOPFXD-VHASINAPPTAVLESDFETVVKLDVPGTYT 1158  
Qy 642 SRVHLIFTSONGEAPFGANFI-----SEIRSEELLSPEL--IKSDAMVGSQGTWIS 692  
Db 1159 --VTTTNEDEGVSAPKEVSVYRKIPAPEITDKEITTPKDEVSBAEFLNDIHATIS 1216  
Qy 693 GNSLINSNVNGTFRONLSIESYSTYSMNFRVNG----- 726  
Db 1217 DKQVAITSN-----FSTDVNLNKA GDYTVTLNATNEDGVKATPVEVIVHQQGERPVITAD 1272  
Qy 727 -----FGKVTITRNSREVVEFSYLOPSSKYSSEKFTTTN 761  
Db 1273 ATISYDKFANITTEKFLIEDIHATISDQSSVTITSNFQTATN 1314

RESULT 4  
US-11-045-004-19  
; Sequence 19, Application US/11045004  
; Publication No. US20060078901A1  
; GENERAL INFORMATION:  
; APPLICANT: BUCHRIEGER, CARMEN  
; APPLICANT: PRANGEUT, LIONEL  
; APPLICANT: COUVE, ELISABETH  
; APPLICANT: RUSNIOK, CHRISTOPHE  
; APPLICANT: FSIHI, HAFIDA  
; APPLICANT: DEHOUX, PIERRE  
; APPLICANT: DUSURGET, OLIVIER  
; APPLICANT: CHETOUANT, PARID  
; APPLICANT: MEDJARI, HAFED  
; APPLICANT: GLASER, PHILIPPE  
; APPLICANT: KUNST, FRANCK  
; APPLICANT: COSSANT, PASCALE  
; APPLICANT: DANIELS, JUSTIN  
; APPLICANT: GOEBEL, WERNER  
; APPLICANT: KREFT, JURGEN  
; APPLICANT: KUHN, MICHAEL  
; APPLICANT: NG, EVA  
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO  
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO  
; APPLICANT: GARRIDO-GARCIA, PATRICIA  
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO  
; APPLICANT: AMEND, ALEXANDRA  
; APPLICANT: CHAKRABORTY, TRINAD  
; APPLICANT: DOMANN, EUGEN  
; APPLICANT: HAIN, THORSTEN  
; APPLICANT: BERCHE, PATRICK  
; APPLICANT: CHARBIT, ALAIN  
; APPLICANT: DURANT, LIONEL  
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO  
; APPLICANT: BAQUERO, FERNANDO  
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO  
; APPLICANT: GOMEZ-LOPEZ, NURIA  
; APPLICANT: MADUENIO, ENCARNIA  
; APPLICANT: PABLOS, BETRIZ DE  
; APPLICANT: WEHLAND, JURGEN  
; APPLICANT: KARST, UWE  
; APPLICANT: EKTIAN, KARL-DIETER  
; APPLICANT: HAUF, JORG  
; APPLICANT: ROSE, MATTHIAS  
; APPLICANT: VOSS, HAMUT  
; TITLE OF INVENTION: *Listeria monocytogenes* genome, polypeptides and uses  
; FILE REFERENCE: 05394.0018-02

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/ CURRENT APPLICATION NUMBER: US/11/045,004
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: 10/637,657
/ PRIOR FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: 10/257,023
/ PRIOR FILING DATE: 2002-10-08
/ PRIOR APPLICATION NUMBER: PCT/FR01/01118
/ PRIOR FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: FR 00/04,629
/ PRIOR FILING DATE: 2000-04-11
/ NUMBER OF SEQ ID NOS: 2854
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 19
/ LENGTH: 1778
/ TYPE: PR1
/ ORGANISM: Listeria monocytogenes
US-11-045-004-19

Query Match      4.4%; Score 175; DB 11; Length 1778;
Best Local Similarity 20.2%; Pred. No. 0.069;
Matches 190; Conservative 140; Mismatches 314; Indels 298; Gaps 50;

QY      4  NNKLS-VKALPSF--IDYFNGIYGFATGIDIMMMFKTMTGGDLT---LDEILKNQOL 56
      487  SNRLSDVSTLTNPSPSLNTYIN-----ISNNVIR--TVGKMTLPSELKFPYAQNNS 533
QY      57  LNEIS-----GKLDGVNGSLNDLAAQNLDTLSKEI-----LKIA 92
      534  ISDISMIDMPNARKVDASNNLTNTGTPNLPKQSLDVHSKRITSTSVIHLPSELETF 593
QY      93  NEQNKLVNDVNT---KLDALNLMNTY-----LPKI-TSMLSDVKNQNYALG-- 135
      594  NAGTNLTNTGMDNLPDLVYVNLSPFRIPSLAPIGLPVLETLIVSDNNSYLRISGTM 653
QY      136 -----LQIEYLS-----KQLKEISDKLDVINNVNLINSTLEIT--PAQRKRYN 179
      654  GVPKARILDQNNYNTMTGTEGNSLSLDTNLTENNNYITIDISGLSTSLRIYLN 713
QY      180 -----EKEEALTSATEYNLKTQDSHTDI--LDELTELTELAKSVTKNDVDFEFLYN 231
      714  LBSNKLIEDISALSNLTNLQELTLENNKINISALSPLNMLKYV--VSKNKI----- 763
QY      232  TRHDVWIGNNLRKRSALKTASL-----LIAXENLKTSGSEVGNVY 271
      764  --IDISPVANMVRGAIIVTASNQTYYTLPTVLSYQSSEFTIDNPYIWDGTLTAPSSIGNSG 821
QY      272  NF---LIIVTALQAKAFLLTTCRKULGLADIDYTIMNHNKKEEPRVNLPLSLNT 328
      822  NYDQKITMTNTMTATSSSTLP-----NEFKLQGL-----TFSGT 856
QY      329  FSNPNYEKARGSDKAKIMEAKPGYALVFEISKDSIALVKYQAKLRH----- 378
      857  VTQP-YKSA-----AKVTADAEQYTT-IGDTISEQF--LQDVNKKSSDGAFTVSDPAT 906
QY      379 -----NYQIDKDSLSEIVYGDIX-----LICPDQSEOMYTTNKIAPENEVY 420
      907  VVDLNTFGEYEVTLTSEKDIQDSCKYVVKVHGAPVISAQT-----ISYDKHAT 958
QY      421  ITRKIAFTKILNS---LRYEVTANFYOSSGTGIDILNKKKIBSSBAEFSMLNANDGYMMI 477
      959  IIEKQPLEDIIHASTDIDTAITTNF--STA-VNLNK-----GGYTVALLNSEMEDGVK-- 1007
QY      478  GTISETEFLPPINGFGLVVDENSRLVTLTKSYLRETLATDLSNKEKTLIVPPNGISNI 537
      1008  ---AETVYVTVT---VNKDPAPIIS-----AKTEIITYDKFSKTEA-----AFLDI 1048
QY      538  ---VENGNLEGENLEBWKANAKAAYDRT-----GGVNGT-KVLVYHEDGSEFSQITG 585
      1049  DADTNDGSLVTSNFA--TAVNLDKAGDYTVTLINSINSDVAGFTPAIIVHVEKE----- 1100
QY      586  DKL-KLKTETVLYOY--IVYKGAAYLKDEKNGDYIYEETNNLE--DEQAVTRKRFITGDS 641
      1101  -KIATISTTAQOYEKYAKINETQFLKD--VHASINASPPTAVLESDFETVVLQDVPGYIT 1158
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QY      642  SRVHLIFTSONGEBAFGNFI-----SEIRPSEELLSPEL--IKSDAMVGSQGTWIS 692
      1159  --VTIATNEDEGVSAAPKREVSIVYKRIAPPELTADKEITYPKREVSSEAFLLNDIATIS 1216
QY      693  GNSLINSNVNNGTFRQNLISLESYSTYSMNPNVNG----- 726
      1217  DKVVAITSN-----FSTDVNLNKRAGDYTVTLNATNEDGVAKATPVEVIVHVOGGRPVITAD 1272
QY      727  -----FGKYTRNSREVVNPFERSYIQFSSKTYISEKFTTTN 761
      1273  ATISYDKFANITYEAKFLIEDIHATISDQSSVTYTSNFOTATN 1314

RESULT 5
US-11-045-004-41
/ Sequence 41, Application US/11045004
/ Publication No. US20060078901A1
/ GENERAL INFORMATION:
/ APPLICANT: BUCHRIEISER, CARMEN
/ APPLICANT: FRANGEUL, LIONEL
/ APPLICANT: COUVE, ELISABETH
/ APPLICANT: KUSNIOK, CHRISTOPHE
/ APPLICANT: FSIHL, HAFIDA
/ APPLICANT: DEHOUX, PIERRE
/ APPLICANT: DUSURGERT, OLIVIER
/ APPLICANT: CHERTOUANI, FARID
/ APPLICANT: MEDJARI, HAFED
/ APPLICANT: GLASER, PHILIPPE
/ APPLICANT: KUNST, FRANCK
/ APPLICANT: COSSART, PASCALE
/ APPLICANT: DANIELS, JUSTIN
/ APPLICANT: GOEBEL, WERNER
/ APPLICANT: KREFT, JURGEN
/ APPLICANT: KUHN, MICHAEL
/ APPLICANT: NG, EVA
/ APPLICANT: VAZQUEZ-BOLAND, ANTONIO
/ APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
/ APPLICANT: GARRIDO-GARCIA, PATRICIA
/ APPLICANT: TIERREZ-MARTINEZ, ALBERTO
/ APPLICANT: AMEND, ALEXANDRA
/ APPLICANT: CHAKRABORTY, TRINAD
/ APPLICANT: DOMANN, EUGEN
/ APPLICANT: HAIN, THORSTEN
/ APPLICANT: BERGE, PATRICK
/ APPLICANT: CHARBIT, ALAIN
/ APPLICANT: DURANT, LIONEL
/ APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
/ APPLICANT: BAQUERO, FERNANDO
/ APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
/ APPLICANT: GOMEZ-LOPEZ, NURIA
/ APPLICANT: MADUENIO, ENCARN
/ APPLICANT: PABLOS, BETRIZ DE
/ APPLICANT: WEHLAND, JURGEN
/ APPLICANT: KARST, UWE
/ APPLICANT: ENTIAN, KARL-DIETER
/ APPLICANT: HAUF, JORG
/ APPLICANT: ROSE, MATTHIAS
/ APPLICANT: VOSS, HAMOTI
/ TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
/ FILE REFERENCE: 05394,0018-02
/ CURRENT APPLICATION NUMBER: US/11/045,004
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: 10/637,657
/ PRIOR FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: PCT/FR01/01118
/ PRIOR FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: FR 00/04,629
/ NUMBER OF SEQ ID NOS: 2854
/ SOFTWARE: PatentIn version 3.3
```

SEQ ID NO 41  
LENGTH: 832  
TYPE: PRT  
ORGANISM: Listeria monocytogenes  
US-11-045-004-41

Query Match 4.4%; Score 174; DB 11; Length 832;  
Best Local Similarity 21.2%; Pred. No. 0.028;  
Matches 157; Conservative 113; Mismatches 269; Indels 202; Gaps 36;

133 ALGQIEVLSKQKLEISDKLDVINNVNLINSTLEIT-----PAYORIKYVNE 180  
Db SLALCFSPVSPSLVASADTITAVOITKEATDTTEPTTIDPQSRMDSQTAPOKWTASS 68  
Qy 181 KFEALTSATE-----TNLTKKQDSSHTDIDELTELTELAKSVTKVDVDFEFLYNTFH 234  
Db 69 EBAATVTSTEEENTPKNNLKSTISNSKT--YAEFPDVNLAKITAKN-IGSTE----- 118  
Qy 235 DVMIGNNLFGSALKTASELIJAKENLKTSGSEGVGVNFIIVLTAQAKAFLLTTCRKL 294  
Db 119 DI---NAVSEAELOITNLVATNQNTS-----LTGIEHL 151  
Qy 295 LGLADITPTIMENHLNKESEFRVNIPTLSNTPSPNPEKANGSDKAKIMEARP-- 352  
Db 152 TALENIN---VNNNELTTIDLFNI---PTLKSISANN--KITGNFSLVKTLPFLHTLB 203  
Qy 353 --GYALVGFEL-SKDSIAVLKVYQAKLKHVQIDKDSLE-----IYGGIDK 397  
Db 204 VLGAITELDLNPNLVLTLSADELEK--KLTLKQLSGLNGLGRIASSISIDWGDES 260  
Qy 398 LACPQSEOMYTTNKIAFPNPEYITKIAFTKQNSLRVEYVAPNFDSTGDIDLNK---- 453  
Db 261 VTLMNLE-----IISVDISGNTDSD--DIHLENLPAV 292  
Qy 454 KTISSSAEFSMLNANDGYMPIGTISEFLPTINGGLVVD--ENSRLVTLTCKSYLR 511  
Db 293 KNLDISNELTRLPKIND--FPL-----LTTINVSNKIDRLSSKLVDPKLTATLN 342  
Qy 512 ETLATLSNKETLIYPPNGFISNIYENGLEGENLEPMKANKNAVYH-----TGV 566  
Db 343 ADKQAVTLS---FTIANGNTIIPNVE--NLAQOMVTPKLIISNGTSDSIIAMAGEL 396  
Qy 567 NG-TKVLVYHED-----GEFSQFIGDKLKTBEVYIYIVKGAIAIY---LKDEK 612  
Db 397 SGLSKSVTDEIVNSPALAKGTGYNQPIEVK---AVPIYADKSVSYAPVNADEAT 453  
Qy 613 -----NGDYIEETNNELEDFQAVTKRPTGTSSRVHL-----I 647  
Db 454 FLQDIRASASENAQITSDY-----SEVDPATPGDYVTLHAKNEFDLKADPTVVVHI 507  
Qy 648 FTSGNGSEAFGNGFIIEIRSEBELLSPELL-KEDAVG---SGGTWISGNSLAINNN 703  
Db 508 NDIOKPPVAVANSNDISFEV--GTELTSEVLLAKSGAVVTDLYDAIKMEVDLSEVDSKL 565  
Qy 704 GTFRONLSLSYSYYS-----MNFNVANGFGKVTIR--NSREVFPRSYLOFSKYSIKET 757  
Db 566 GTREATIIAKSKGASSDPIKLSVKIYDTEKPTIIQINNPETIIEKSELBGOIIDVGI 625  
Qy 758 TTTNN---TGLVVELSRASS 774  
Db 626 TATDNYDQDLNIMHDLISKVDY 646

RESULT 6  
US-10-878-556A-169  
Sequence 169, Application US/10878556A  
Publication No. US20050266399A1  
GENERAL INFORMATION:  
APPLICANT: Hoffmann La-Roche Inc.  
TITLE OF INVENTION: HCV regulated protein expression  
FILE REFERENCE: 21762  
CURRENT APPLICATION NUMBER: US/10/878.556A  
CURRENT FILING DATE: 2004-06-28

NUMBER OF SEQ ID NOS: 199  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 169  
LENGTH: 1404  
TYPE: PRT  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: humanp/chr12-q14221  
DATABASE ENTRY DATE: 2003-04-22  
US-10-878-556A-169

Query Match 4.2%; Score 168.5; DB 9; Length 1404;  
Best Local Similarity 21.3%; Pred. No. 0.12;  
Matches 146; Conservative 111; Mismatches 272; Indels 157; Gaps 29;

Qy 31 DINAMIFKTNVGDLTLDLIELIKNOQLNEISGKLDGVNGSLINDILAO-GNLDTELS--KE 87  
Db 657 DLQNH-----DTAQNALQDQOEINLKITTDQVYAKLQDQEHCSQLESHLKEYKE 709  
Qy 88 ILKIANQNVNDVNTKLDALINMLNTYLPKITSMLSDVMKQVYALGLOIEVLSKOL-- 145  
Db 710 KYLSLEQTEBLEQIKLELADSLVAKSKQALQDQORQLNTDLELRATELSKQLEM 769  
Qy 146 -KEI--SDKLDVINNVNLINSTLEITPAYORIKYVNEKEBALTSATEYMLTKQDSSHT 202  
Db 770 EKEIVSTRDLQKKSALASIKQKLTQKEBEKILKQDETLSQETKI-----QHE 821  
Qy 203 DILDEL-TELTELAKSVTKVDVDFEFLYNTFHDVMI GNNLFGSALKTASELIJAKENL 261  
Db 822 ELNNRIQTIVTELOK--VKMEKEALMTELSTVDKLSKVS---DSLKNSKSEPEKENOK 875  
Qy 262 TSGSEGVNVNFIIVLTAQAKAFLLT--TCRKLGLADIDYTPIMENHLNKESEFRV 320  
Db 876 GKA-----ALDLEKCKEELK-----HOLQVOMENTLKQKLEKKS 911  
Qy 321 ILPTLSNTPSPNPEKANGSDKAKIMEARPGYALVGFESKDSIAVLKVYQAKLKHNY 380  
Db 912 L-----EKEKASHQKL-----ELNSQEBOLQA-QNTLAKONE 944  
Qy 381 QIDKDSLEIYVGDIDKLCPPQSEOMYTTNKIAFPNPEYITKIAFTKQNSLRVEYV 440  
Db 945 KEEQO-----LQGNINEL--KQSEBQKKQIEALQELKIAVLQTELNLKQOQVLT-- 994  
Qy 441 FVDSSTGIDILANKKIESSSAEFSMLNANDGYMPIGTISEFLPTINGGLVVDENSR 500  
Db 995 ---QAAQELAAEKEL-----SVLQNNYE-----KSQETFKQLOQSDP----- 1028  
Qy 501 LVTLTCKSYLRET-LIAT--DLNKEETKLIYPPNGFISNIYENGLEGENLEPMKANKN 557  
Db 1029 -----YGRSEELATRDQLKSVBEKLSLAQEDLISNNQIGN-QNKLIQELKTAKAT 1079  
Qy 558 AYYDHGTGVNGTVLVYHEDSEFSQFIGDKLKTBEVYIYIVKGAIAIY---IYLKDEK 613  
Db 1080 LEQD-----SAKKEQOQOEKCKALQDIOREKSLKEKELVN--EKSCLAEIEIKCRQKE 1132  
Qy 614 GDYIEETNNELEDFQAVTKRPTGTSSRVHL-----FTSGNGSEAFGNGFI 661  
Db 1133 ---ITKNEELSHKLESIKETITNLKDAQQLIIQKLELOGRADSIKAAVEQEKRNQOI 1188  
Qy 662 IIEIRSEBELLSPELLKSDAVGSGQ 687  
Db 1189 LKQVQKKEBELEKKEFEIKEKAKLHSE 1214

RESULT 7  
US-11-045-004-1251  
Sequence 1251, Application US/11045004  
Publication No. US20060078901A1  
GENERAL INFORMATION:  
APPLICANT: BUCHRIEISER, CARMEN  
APPLICANT: FRANGEUL, LIONEL  
APPLICANT: COUVE, ELISABETH  
APPLICANT: RUSNIOK, CHRISTOPHE

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APPLICANT: FSIH, HAFIDA
APPLICANT: DEHOUX, PIERRE
APPLICANT: DUSSENET, OLIVIER
APPLICANT: CHETOUANI, FARID
APPLICANT: NEDJARI, HAFED
APPLICANT: GLASER, PHILIPPE
APPLICANT: KUNST, FRANCK
APPLICANT: COSSART, PASCALE
APPLICANT: DANIELS, JUSTIN
APPLICANT: GOEBEL, WERNER
APPLICANT: KREFT, JURGEN
APPLICANT: KUHN, MICHAEL
APPLICANT: NG, EVA
APPLICANT: VAZQUEZ-BOLAND, ANTONIO
APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
APPLICANT: GARRIDO-GARCIA, PATRICIA
APPLICANT: TERRERZ-MARTINEZ, ALBERTO
APPLICANT: AMEND, ALEXANDRA
APPLICANT: CHAKRABORTY, TRINAD
APPLICANT: DOMANN, EUGEN
APPLICANT: HAIN, THORSTEN
APPLICANT: BERCHER, PATRICK
APPLICANT: CHARBIT, ALAIN
APPLICANT: DURANT, LIONEL
APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
APPLICANT: BAQUERO, FERNANDO
APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
APPLICANT: GOMEZ-LOPEZ, NURIA
APPLICANT: MADUENIO, ENCARNIA
APPLICANT: PABLOS, BETRIZ DE
APPLICANT: WEHLAND, JURGEN
APPLICANT: KARST, UWE
APPLICANT: ENTIAN, KARL-DIETER
APPLICANT: HAUF, JORG
APPLICANT: ROSE, MATTHIAS
APPLICANT: VOSS, HAMUT
APPLICANT: TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
FILE REFERENCE: 05394.0018-02
CURRENT APPLICATION NUMBER: US/11/045, 004
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: 10/637,657
PRIOR FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: 10/257,023
PRIOR FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: PCT/FR01/01118
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: FR 00/04,629
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 2854
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1251
LENGTH: 896
TYPE: PRF
ORGANISM: Listeria monocytogenes
US-11-045-004-1251

```

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Query Match 4.2%; Score 166.5; DB 11; Length 896;
Best Local Similarity 20.1%; Pred. No. 0.082;
Matches 129; Conservative 106; Mismatches 224; Indels 183; Gaps 31;

27 TGKIDIMNMFK--TNTGDDLTLDEI-----LKNQ-QLNLISGRLDGVNGLSNDLQA 77
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
156 SGATTIVNQISSFEVGTASKAVLEEFNKAIGIDLENBLPTIRLKTGVFVQDALPELKKM 215
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
78 GNLDTLSLSEILKIANEOKKVLNDVTKLDAIN-----LMNTYIPKITSMLSDVMKCN 131
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
216 GAEAVIEAKLPBLKKAQV--ELNEKIPBLNKATENVLVEOQLPKIDOLGODILVLAQ 274
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
132 VALGQIEYISKOLKEISDKLDVY--NVNVLIN-----STLSEIIPAPORIKY---- 177
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
275 KKLIP-ELIKOIASVVEVDENFGITKKTVDAYANESGKALDVIDTAMAAIPYVEKIAQNS 333
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
178 -----VNEKFEALTSATETNLKTQDSSHTDILDELTE-----LTE 213

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DB 334 GYVDKXSDFADEINKSFDTLAPAIKQNTLTKQMA--DNIVQTEAIKNGSTTPEQATITE 391
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 214 LAKSVTKNDVDGEFFYLNTHFDVMIQNNLFGSAL-----KTASBLIAKENLKTSGSEV 267
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 392 LKK--MEODIDSLQ-----OMITQFATLSLNEBTLPNKRPFDTLIA--NLKTINSQL 439
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 268 GNYNPLIVLTLAQAKAFLLTTCRKLGLADIIDYPIPMHEHLNKEKEPRVNVILPLSN 327
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 440 G-----AQKE--TITVR-----TELENGAQSEELNLNLEQAKVSEKLDQ 480
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 328 TFSNPVYKARGSDKDKAKIIMEAKPGYALVGFSEISKDSIALVLKVYQAKLKHNYQIDKSD 387
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 481 ILAN-----YSEIYPAIKVGLNQIGDL-KDSQKLETLQAKIPEITQVYKDSR 529
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 388 SEIYVG-----DIDKLLCPDQSEQMYTNRKIAFPNEYVITTKIAFTKNSLR 435
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 530 ETLQGTQYLEBFQERLPEIQKTL--DEA-----TKVIINT-KLDTIITA 569
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 436 EV--TANFYDSSIGDIDLNKKIESSEAFESMLNANDGVYMPIGTISEFLTPINGFL 493
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 570 GINEAANFYQNDYPNKANIK--AANF-----IRDDLPLEK 605
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 494 VVDENSLVTLTCKSYLRETLATDLSNKEKTLIVPNGFISNIYENGNILEGENTLPPWKA 553
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 606 EINQASGLIOEKMPFEKAIKIAADLSRE--LPE--FEKAIYN-----A 646
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 554 NKNAYVDHTGGVNGTKVLVYHEHGEFSQFIDKTLK--TEY 594
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 647 ANKITDFDKNYDLOSIIKMLRNDADKSSFIASPVLKETS 688
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 8
US-10-909-769-24
Sequence 24, Application US/10909769
Publication No. US20060024331A1
GENERAL INFORMATION:
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Lin, Wei-Jen
APPLICANT: Aoki, Kei Roger
APPLICANT: Sachs, George
TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characteristic
FILE REFERENCE: ALB0010-100 (R012003-146)
CURRENT APPLICATION NUMBER: US/10/909,769
CURRENT FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.3
SEQ ID NO 24
LENGTH: 834
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Amino acid sequence of HC
US-10-909-769-24

```

```

Query Match 4.1%; Score 163.5; DB 9; Length 834;
Best Local Similarity 19.7%; Pred. No. 0.11;
Matches 170; Conservative 114; Mismatches 274; Indels 305; Gaps 38;

16 IDYFNGIYGFATGIDIMNM-----IFKTVNGGDLTJLDELKNOQLNE 59
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 126 LQYSKITTFTPLSLKRNKGVQAGLFLANWANEVVEDTTINIMKQDTLCKSDSVSVITPY 185
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 ISGKLD---GVNGSLNDLAQNLDT-----TELSKEILKI-----ANEQNKYLANDVN 103
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 186 IGPALNIGSALRGFNQAFATGAVAFLLGEPPEFTIPALGVFTFYSSIQEREKIKITIE 245
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 104 TGL-----DAITLMTNTYIPKITSMLSDVMKKNYVALGQIEYLSQKLEISDKLDVY 155
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 246 NCLEGRVAKWDSYQWMSNMLSRITTFQHNINQMY-----DSLVSQAQAIKAKIDL- 298
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 156 NVNVLINSTLFEITPAQYRIKYVNEKFEALTSATETNLKTQDSSHTDILDELTE----- 210

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Db 476 DKVL-----XIKENSNVITSOKVTVASQLTQGVKVENSLSSKEYI-- 522
Qy 452 NKKKIESSEAFSMANNDGVWPIGTI-----SETFLPTINGGLV 494
Db 523 -----IEMELLVDGKAVTDGMYFISSTLAKPTIEGLNLSYSTDKGEFVASPVN---L 574
Qy 495 VDENSRLVLTCKSYLRETLATDLSNKEKTLVPPNGFISNIVEGNLEGENLEPKAN 554
Db 575 VDRDEITSIRYAVLEDDYKVGNSNAKEYASVVDANQKKTAKVGRITVDMN-----D 628
Qy 555 NKAYVHTGNGVGTKLYLHEDGESEQFIDKLLKTEYVIQYVKGAAI----- 606
Db 629 GNVTFVGISGNGQSDYTPATPASNSVVGKTKTPVEFSLKEAEQDKLTINVEYVAD 688
Qy 607 -----YLDEKNGDVIYEITNNELEDFOAVTKRFTI-----GTDSSRVHL 646
Db 689 NTLFEDVLTHPTLKLKYSDAQGY-----SGNPVATVDLTCKSDITNLEFDGSESAIYV 744
Qy 647 IFTSQNGEAFGGNFIIE-IRPSEELLSPELIKSDAMVGSOGTWISGNSLANSVNGT 705
Db 745 VWTGSYNLDDAGIMVDELIGOSSVFRTEITK-----VNAS 782
Qy 706 FRONLSIESYTSYMANNNV-GFGKVTIRNSREVVERSYLOPSKTI-----EKF 756
Db 783 F-----SLDSVDYTKKVALNVKLSDAVNLANDANKIYEKK-----TNLTAKTVPLHGFEL 834
Qy 757 TTTTNNGLYELS 770
Db 835 MSDSGNSYLFENIS 848

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RESULT 10
US-10-793-626-1780
; Sequence 1780, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 1780
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1780

```

```

Query Match 4.0%; Score 161.5; DB 9; Length 1155;
Best Local Similarity 18.5%; Pred. No. 0.22;
Matches 170; Conservative 136; Mismatches 285; Indels 327; Gaps 46;
Qy 47 LDEILNQQQLNIEISGKLDGVNSLNDLLAQLDTELSK-----ELKLANEQ 95
Db 309 INEATIAELKDKDPSPDYGVDPPL-----ALNTSQSKNSPKKASPRMIMLSIAAE 361
Qy 96 NKVLNDVNTKLDALINIMLNTYLPKITSMLSDV-----MKQYAL----- 134
Db 362 NSGKN-VNKKVKTNTTLS--LNKSNHANNVWPTSNGQFUKANYTELDDISKEGDTT 418
Qy 135 -----GLQIEYLSKQLKEISDKLDVINNVNLINSTLTETPAYGRIKYVEKFEA 184
Db 419 IKYGYIRPGLELPAIKTQLR---SKDGIYANGVYDKTYN--TTTYFTYVY-DQYON 472
Qy 185 LMSATETNKTQDSSHTIIDLTELTLTBLAKSVYTKND--VGFEPYALTFHDWIMGNL 242

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Db 473 ITGSPDLIATPKKRETAIKONQNYPMETV--IANEVKKDFIVD-----YGNK- 517
Qy 243 FGRSALKTASELAKENMLKTSSEGVGNVNFILVTLAQAKALTLTTCRKLGLADIDY 302
Db 518 -----KON--TTTAAVANVDN----- 531
Qy 303 TPIINHELNKEKEEFVNILPTLSNTPSNPNYKARGSPKDAKIMEAKGYALVGEFIS 362
Db 532 --VNNH-----NEVVYLNQNNQNPKAKYISTYKNGFET---PGEKVY-YEYI 574
Qy 363 KDSIAVLKYYQAKLKNNYQIDKDSLEIYGGIDKLLCPDQSEOMYTYNKLAPNEYVT 422
Db 575 -DTNANVDSF-----NPDLSNVADVTYSQFTPKVASADGTRVDINFARSMANGKKYIV 627
Qy 423 KLAFTKKLSLRYEV-----TANFY-----DST-----GD----- 448
Db 628 QAVRPTGTGVVTEYWLTRDGTNTNDFRGYKSTTVTYLNGSSTAQGNPTYSLADYVW 687
Qy 449 IDLNKKKI-----ESSEAFSMANNDGVY-----MPIGTISEFTPLPI 488
Db 688 LDKNKGVODDDEKGLAGYVTLKDSNRELQRVTTDQSGHQFDNLQNGTYTVERAID 747
Qy 489 NGFGLVDENSRLVLTCKSYLRETLATDLSNKEKTLVPPNGFISNIVEGNLE-GEN 547
Db 748 N-----YTPSPANNSTNDALDSGDERDGRKVVAKGTLNN--ADNMVVDYGFY 794
Qy 548 LEP-----WKANNKNAVY-DHICGVNGTVLYLHEDGEF-----SOFIDGK 587
Db 795 LTPKTVNGDYVEDTKDGIQDDNEKGISNVKTVLKNKGDYITGTTTDSNGKYEFTGLE 854
Qy 588 LKLKTEYVIQYIVK-----GKAIFYLDEKN----- 613
Db 855 ---NGDYTLEFEPFBEGYPTTKQNSGDEKDSNGKTYTVTVADANKTIDSGFYKPIYVL 911
Qy 614 GDYIYEITNNELEDFOAVTKRFTIET-----DSSRVHLFTSQNGEAF---GNGFI 662
Db 912 GDYVEDTYNK--DGIDQDEKGISGVKTVLKDKNGALIGTTTDSGHHQFGLGEGSYT 969
Qy 663 ISEIRPSEELLSPELIKSDAMVGSOGTWISGNSLANSVNGTFRONLSLE--YST-Y 718
Db 970 VEEETPSG--YTPYKANS-----GQDIYVDSGITTGTIINCA--DNLITDSGFYKTPKY 1020
Qy 719 SM-----NFWNGFG--KVTIRNSREVVERSYLOPSKTISEKFTTTNN 762
Db 1021 SVGDYVEDTNKDGQDDNEKGISGVKTVLKDEKNNIIS-----ITTTDE 1065
Qy 763 TGLYELSPASSRGVINF 780
Db 1066 NCKYQFDNLDSGNVYIHF 1083

```

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RESULT 11
US-11-079-463-5584
; Sequence 5584, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 5584
; LENGTH: 1249
; TYPE: PRT
; ORGANISM: B. fragilis
US-11-079-463-5584

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Db 1234 LNCIAGSNAQVIHVNISIALGNGSTTTRGAQNTYATYANMDAPONSVEFSV 1284

RESULT 13

US-11-123-241-125

/ Sequence 125, Application US/11123241

/ Publication No. US2006078565A1

/ GENERAL INFORMATION:

/ APPLICANT: Microbial Technics Limited

/ APPLICANT: Le Page, Richard WF

/ APPLICANT: Wells, Jeremy M

/ APPLICANT: Hamifly, Sean B

/ TITLE OF INVENTION: Proteins

/ FILE REFERENCE: PWC/P21089w0

/ CURRENT APPLICATION NUMBER: US/11/123,241

/ CURRENT FILING DATE: 2005-05-06

/ PRIOR APPLICATION NUMBER: US/09/769,736

/ PRIOR FILING DATE: 2003-02-14

/ PRIOR APPLICATION NUMBER: GB 9816335.5

/ PRIOR FILING DATE: 1998-07-27

/ PRIOR APPLICATION NUMBER: US 60/125163

/ PRIOR FILING DATE: 1999-03-19

/ NUMBER OF SEQ ID NOS: 212

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 125

/ LENGTH: 903

/ TYPE: PRT

/ ORGANISM: Streptococcus agalactiae

US-11-123-241-125

Query Match 4.0%; Score 159.5; DB 11; Length 903;

Best Local Similarity 19.2%; Pred. No. 0.21;

Matches 140; Conservative 104; Mismatches 298; Indels 187; Gaps 30;

QY 83 ELSKEILKIAN-----EENKVLNDVNTKLDALINMLNTYLPKITSMLSDVWKQNYALG 135

DB 159 EDTKEVYPLVNVGSKVGEQYKALNPNGK-DGRREIAGCGLSKKPGVNDLQNKYKIE 217

QY 136 IQIE-YLSKQKEISPKLDVINNVVLINSTLTETPAVQRIKYVNEKEFALTSATETNLK 194

DB 218 LTVGKTYVETKELNGLDVLVLDNSNMNERANSQALAGAEVETL-----268

QY 195 TKODSHTDILDELTELTELAKSVTYNDVDGFEFYINTFHDVMI GNNLFGRSALKTASEI 254

DB 269 -----IDKITS-----NKDNRYALVTASTIFD-----GTEA--TVSKG 300

QY 255 IAKENLKTSGSEVGNVNFILVLTALQAKAFLLTTCRKLLGLADIDYTPIMNEHLANKER 314

DB 301 VADQNGKALNDVSMWDYHKTFTATTHTNYSYLVLTN-----DANEVNIILKSRI PKEA 352

QY 315 EEFRRV-ILPTLSNTEFSNPYERKA-----RGSDDKAKIIMEAKPGVALVGFETSKDSTA 367

DB 353 EHNIGRRTLYQFQATFTQKALMAGANLEIETQSSNAKKLIFHTDGVPTMSYALN-----407

QY 368 VLKTYQAKLKHNYQIDKDSISEIYVGDIDKLLCPDQSEQMYTNTKIAFPNEYVITKIAFT 427

DB 408 -----FNPYISTSYQNFNS-----FLNKL--FDRSGIILQEDFI 439

QY 428 KKLNSLRVEVTANFYSSSTGDDIDLANKKIESSAEFSMLNANDGYVMP--GTISETL 485

DB 440 --INGDYOI-----YKGDSESKLPSDRK---VPTVGTITQAAAR 475

QY 486 TPIINGGLVND-----NSRLVLTTCCKSYLRETLATDLSNKETKLI--VPNPGFINIYE 539

DB 476 VPONQSVSNBEGYALNSGVIYIYMPDY--NMWYPPDPKTKKYSATKQIKTHSEPTLVF 533

QY 540 NGNLEGENLEPWKANKKAYVDHTGCVNGTKVLVYHDEGFSQFIGDKLKTKEYVIOYI 599

DB 534 NGNIRPKGYDIFVTGI-----GVNBDPGATPLEAEKMQSISKTENTYTNV-----579

QY 600 VAGKAIYIKDEKNGDGYIYEETNNELEDYQAVTKRITG--TDSRVHLIFTSQNGBEAF 657

DB 580 -----DDTN--KIYDELNKKYPTKTYVEKHSIVDGNVTDPMGEMTEFOLKNGQSF 627

QY 658 GGNFIISIRPSELLPBLIKSDAWVSGQGTWISGNSLINSNVNGTFRONLSESYST 717

DB 628 HDDYVL-----VANDSGQLKNGVALGGBPNQGLIKQVTV--TYRK 666

QY 718 YSMNFVNGPGKYTTIRNSREVVPERSY-LQFSKYSISEFTTTTNTNGLYVELSRASSRG 776

DB 667 TSQTITKIN--HNLISGQKRVL--TYDVLKDNYSNKFYNTNNT-----TLPKSEKE 717

QY 777 VINFGDPSI 785

DB 718 PNTIRDPFI 726

RESULT 14

US-10-793-626-2964

/ Sequence 2964, Application US/10793626

/ Publication No. US20050255478A1

/ GENERAL INFORMATION:

/ APPLICANT: KIMMERLY, WILLIAM JOHN

/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

/ FILE REFERENCE: PUS480US

/ CURRENT APPLICATION NUMBER: US/10/793,626

/ CURRENT FILING DATE: 2004-03-04

/ PRIOR APPLICATION NUMBER: 60/164,258

/ PRIOR FILING DATE: 1999-11-09

/ NUMBER OF SEQ ID NOS: 4472

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 2964

/ LENGTH: 5024

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Description of Artificial Sequence: synthetic

/ NAME/KEY: MOD RES

/ LOCATION: (5024)

/ OTHER INFORMATION: variable amino acid

US-10-793-626-2964

Query Match 4.0%; Score 159.5; DB 9; Length 5024;

Best Local Similarity 20.4%; Pred. No. 2.2;

Matches 156; Conservative 116; Mismatches 283; Indels 211; Gaps 36;

QY 3 KNNKLSYKALPSEFIYFNGIYGFATGIDIMMIRKTYNGDLTJDEILAKNOQLNEISG 62

DB 4159 ESNSTSV--PNSVNTINADKNVLQIEFDEALQOASATSS-----KTSNPATIEEVLG 4208

QY 63 KLDGVGSLNDLLAOGNLDTELSKE--ILKIANEQNKV-LNDVNTKLDALINMLN--TYVP 118

DB 4209 LQOATYDTGNALNGGQRATETSKDOLKILKGLKDLNKQLEBVTYKVNANLITELSQLT 4268

QY 119 KITSMLSDMK-----QNYALGLQIEYLSKQLEISDKLDVINV 157

DB 4269 QSTLKLNDKMKCLRDKLTLPVVPKASLRYRNADYNLKRQFPAKLEAGVNLKSGTIV 4328

QY 158 NVL-INSTLTETTPA-----YQRIKYVNEKEE-----ALTSATETNLTKQD 198

DB 4329 NINDIOLHTQIDNKAQDOLNGERRUKERHQKSEVEPIKELDIINNAQKAAIINQIRASQD 4388

QY 199 -----SSHTDIDELTELTELAKSVTKNDVDGFEFYINTFHDVMI GNNLFGRSALKT 250

DB 4389 IKTIQIYDNLAEIANDMAGLKEHVAQLTATTQKNIE--YLNADDELKIQYD-----AIVL 4443

QY 251 ASELIAKENLKTSGSEVGNVNFILVLTALQAKAFLLTTCRKL--GLADIDYTPIMNEH 309

DB 4444 ANNVLDKEN-----GTNKDANIIIGMIQ-----NMDDARALLNGI-----ER 4480

QY 310 LNKEKEEERVNLILPTLSNTEFSNPYERKAGSGK-DAKIIM--EAPPGVALVGFETSKSI 366

DB 4481 LMDAQTKAHNDIKDILKQOLDEIEHANATNSKQAKQKQMVNEAKRAPSINIHATSNL 4540



```
OY 697 NINNVNCTFR-QNISLESYS-----TYSNPNVNGFGKVTIRNSREVVFRSYLOF 747
    | : : | | | : : | | | : : |
Db 1208 NLTTDANGELITVTNLAPGKYSFKETKAPGEYELATDVWEF---TIAPNQ----- 1253
OY 748 SSKYISEKFTTTNNYGL 765
    | | | | | | | |
Db 1254 -----PEKITTTAENTKL 1266
```

Search completed: May 15, 2006, 20:48:27  
Job time : 34 secs

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 15, 2006, 20:48:06 ; Search time 188 Seconds  
(without alignments)  
1836.977 Million cell updates/sec

Title: US-10-698-096-17

Perfect score: 786  
Sequence: 1 MQRNNKLGVXALPSPFIDYFN.....VELSRASSRGVINGDFPSIK 786

Scoring table: **ODTGO**  
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size 8 1

Total number of hits satisfying chosen parameters: 2442881

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: Geneseq\_21.\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	5.9	787	7 ADD43701	Add43701 Bacillus
2	45	5.7	787	3 AAY59284	Aay59284 SUB toxin
3	45	5.7	787	8 ADG88542	Adg88542 Bacillus
4	43	5.5	511	2 AAW46865	Aaw46865 Bacillus
5	43	5.5	511	2 AAY24968	Aay24968 Bacillus
6	43	5.5	759	2 AAW46864	Aaw46864 Bacillus
7	43	5.5	759	2 AAY24967	Aay24967 Bacillus
8	43	5.5	786	7 ADD43705	Add43705 Bacillus
9	43	5.5	787	6 ABB82567	Abb82567 B. thurin
10	43	5.5	787	6 ABB82565	Abb82565 B. thurin
11	43	5.5	787	6 ABB82565	Abb82565 B. thurin
12	43	5.5	787	7 ADN08758	Adn08758 B. thurin
13	43	5.5	788	7 ADD43703	Add43703 Bacillus
14	43	5.5	788	7 ADN08783	Adn08783 B. thurin
15	43	5.5	789	2 AAW60216	Aaw60216 Bacillus
16	43	5.5	789	2 AAW60217	Aaw60217 Bacillus
17	43	5.5	789	2 AAW46862	Aaw46862 Bacillus
18	43	5.5	789	2 AAW46863	Aaw46863 Bacillus
19	43	5.5	789	2 AAW46868	Aaw46868 Bacillus
20	43	5.5	789	2 AAW46867	Aaw46867 Bacillus
21	43	5.5	789	2 AAW46866	Aaw46866 Bacillus
22	43	5.5	789	2 AAW46866	Aaw46866 Bacillus
23	43	5.5	789	2 AAW46861	Aaw46861 Bacillus
24	43	5.5	789	2 AAY24971	Aay24971 Bacillus

25	43	5.5	789	2 AAY24966	Aay24966 Bacillus
26	43	5.5	789	2 AAY24970	Aay24970 Bacillus
27	43	5.5	789	2 AAY24974	Aay24974 Bacillus
28	43	5.5	789	2 AAY24972	Aay24972 Bacillus
29	43	5.5	789	2 AAY24965	Aay24965 Bacillus
30	43	5.5	789	2 AAY24964	Aay24964 Bacillus
31	43	5.5	789	2 AAY24969	Aay24969 Bacillus
32	43	5.5	789	6 ABB82566	Abb82566 B. thurin
33	43	5.5	789	7 ADN08756	Adn08756 B. thurin
34	43	5.5	790	2 AAW60215	Aaw60215 Bacillus
35	43	5.5	790	2 AAW6872	Aaw6872 Bacillus
36	43	5.5	790	2 AAW46871	Aaw46871 Bacillus
37	43	5.5	790	2 AAY24975	Aay24975 Bacillus
38	43	5.5	790	3 AAY59275	Aay59275 Toxin fro
39	43	5.5	790	8 ADG88492	Adg88492 Bacillus
40	41	5.2	789	2 AAW46860	Aaw46860 Bacillus
41	41	5.2	789	2 AAY24963	Aay24963 Bacillus
42	38	4.8	788	7 ADN08753	Adn08753 B. thurin
43	35	4.5	789	2 AAR91243	Aar91243 B. thurin
44	35	4.5	789	2 AAW19514	Aaw19514 B. cereus
45	35	4.5	789	2 AAW46725	Aaw46725 Vegetativ

#### ALIGNMENTS

RESULT 1  
ADD43701  
ID ADD43701 standard; protein; 787 AA.  
XX  
AC ADD43701;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Bacillus thuringiensis insecticidal protein ISP3-1099E.  
XX  
KW Insecticidal; plant insect pest; pesticide.  
XX  
OS Bacillus thuringiensis.  
XX  
PN WO2003080656-A1.  
XX  
PD 02-OCT-2003.  
XX  
PF 20-MAR-2003; 2003WO-EP003068.  
XX  
PR 22-MAR-2002; 2002US-0366276P.  
PR 06-NOV-2002; 2002US-0423999P.  
XX  
PA (PARB ) BAYER BIOSCIENCE NV.  
XX  
PI Arnaut G, Boets A, De Rudder K, Vanneste S, Van Rie J;  
XX WPI; 2003-876903/81.  
XX DR N-PSDB; ADD43700.  
XX  
PT New insecticidal proteins, useful for controlling plant insect pests, and  
PT for increasing resistance to insect damage compared to control plants.  
XX  
PS Claim 3; SEQ ID NO 2; 81bp; English.  
XX  
CC The present invention relates to Bacillus thuringiensis insecticidal  
CC proteins (ADD43701, ADD43703 and ADD43705) and their coding sequences  
CC (ADD43700, ADD43702 and ADD43704). The insecticidal proteins are  
CC insecticidal against Helicoverpa zea, Heliothis virescens, Ostrinia  
CC nubilalis, Spodoptera frugiperda, Agrotis ipsilon, Pectinophora  
CC gossypiella, Scirphophaga incertulanis, Gnathocoridis medialis, Sesamia  
CC inferens, Chilo partellus and Anticarsia gemmatilis. The proteins are  
CC useful for controlling plant insect pests, and for increasing resistance  
CC to insect damage compared to control plants.  
XX  
SQ Sequence 787 AA;

Query Match 5.9%; Score 46; DB 7; Length 787;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-39;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 514 LLAATDSNKEIKLIVPENGFSINIVENGLENLEPDKANNKNAY 559  
 DB 515 LLAATDSNKEIKLIVPENGFSINIVENGLENLEPDKANNKNAY 560

RESULT 2  
 ID AAY59284 standard; protein; 787 AA.  
 XX AAY59284;  
 AC AAY59284;  
 XX  
 DT 18-APR-2000 (first entry)  
 XX  
 DE SUP toxin from B. thuringiensis strain KB59A4-6.  
 XX  
 KM Bacillus thuringiensis; toxin; endotoxin; pesticide; plant pest;  
 KW Lepidoptera; coleoptera.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 PN WO957282-A2.  
 XX  
 PD 11-NOV-1999.  
 XX  
 PF 06-MAY-1999; 99WO-US009997.  
 XX  
 PR 06-MAY-1998; 98US-00073898.  
 XX  
 PA (MYCO ) MYCOGEN CORP.  
 XX  
 PI Feltelson JS, Schepf HE, Narva KE, Stockhoff BA, Schmeits J;  
 PI Loewer D, Dullum CJ, Muller-Cohn J, Stamp L, Morrill G;  
 PI Finstad-Lee S;  
 XX  
 DR WPI; 2000-096811/08.  
 DR N-PSDB; AAZ58823.  
 XX  
 PT New polynucleotides encoding pesticidally active proteins, useful for  
 PT transforming plants for controlling pests.  
 XX  
 PS Claim 2; Page 100-103; 104pp; English.  
 XX  
 SS The invention relates to novel B. thuringiensis isolates, and genes  
 CC encoding pesticidal toxins which are toxic to non-mammalian pests. The  
 CC genes are useful in the control of non-mammalian pests and especially  
 CC plant pests (e.g. lepidoptera and/or coleoptera). The polynucleotides  
 CC are useful for transforming plants for controlling plant pests; for  
 CC designing primers and probes useful for the identification and  
 CC characterization of genes which encode pesticidal toxins. The present  
 CC sequence represents a B.t. SUP toxin  
 XX  
 SQ Sequence 787 AA;

Query Match 5.7%; Score 45; DB 3; Length 787;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-38;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 EYLSKQLKEISDKLDVINNVVLINSTLTETTPAYORIKYVNEKFE 183  
 DB 140 EYLSKQLKEISDKLDVINNVVLINSTLTETTPAYORIKYVNEKFE 184

RESULT 3  
 ID ADG88542 standard; protein; 787 AA.  
 XX ADG88542;  
 AC ADG88542;  
 XX  
 DT 11-MAR-2004 (first entry)

XX  
 DE Bacillus thuringiensis strain KB59A4-6 SUP toxin protein.  
 XX  
 XX Pesticide; genetic engineering; resistance; toxin; insecticide;  
 KW plant protectant; gene; ds.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 PN US603063-B1.  
 XX  
 PD 05-AUG-2003.  
 XX  
 PF 07-MAY-1999; 99US-00307106.  
 XX  
 PR 07-MAY-1999; 99US-00307106.  
 XX  
 PA (MYCO ) MYCOGEN CORP.  
 XX  
 PI Feltelson JS, Schepf HE, Narva KE, Stockhoff BA, Schmeits J;  
 PI Loewer D, Dullum CJ, Muller-Cohn J, Stamp L, Morrill G;  
 PI Finstad-Lee S;  
 XX  
 DR WPI; 2004-008371/01.  
 DR N-PSDB; ADG88541.  
 XX  
 PT New polynucleotide from Bacillus subtilis, which encodes delta endotoxins  
 PT or pesticide proteins, useful in plant genetic engineering, particularly  
 PT for producing plants that are resistant to lepidopteran or coleopteran  
 PT pests.  
 XX  
 PS Claim 1; SEQ ID NO 54; 51pp; English.  
 XX  
 SS The present invention provides an isolated polynucleotide from Bacillus  
 CC thuringiensis (B.t.) strain KB59A4-6 that encodes an active pesticidal  
 CC SUP toxin protein. The invention is useful in plant genetic engineering  
 CC particularly producing plants that express such gene in order to  
 CC effectively control various insects e.g. boll weevil, black cutworm etc.  
 CC The invention is also useful for conferring resistance in plants against  
 CC lepidoptera or coleoptera. The present sequence is Bacillus  
 CC thuringiensis protein.  
 XX  
 SQ Sequence 787 AA;

Query Match 5.7%; Score 45; DB 8; Length 787;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-38;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 EYLSKQLKEISDKLDVINNVVLINSTLTETTPAYORIKYVNEKFE 183  
 DB 140 EYLSKQLKEISDKLDVINNVVLINSTLTETTPAYORIKYVNEKFE 184

RESULT 4  
 ID AAW46865 standard; protein; 511 AA.  
 XX AAW46865;  
 AC AAW46865;  
 XX  
 DT 11-JUN-1998 (first entry)  
 XX  
 DE Bacillus thuringiensis toxin designated 94R1(a).  
 XX  
 KM Toxin; lepidopteran pest; control; Agrotis ipsilon; black cutworm;  
 KW Heliothis virescens; Helicoverpa zea.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 PN WO9800546-A2.  
 XX  
 PD 08-JAN-1998.  
 XX  
 PR 01-JUL-1997; 97WO-US011658.  
 XX  
 PF



PR 01-JUL-1996; 96US-00674002.  
XX  
XX (MYCOG) MYCOGEN CORP.  
XX  
PI Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;  
XX  
DR WPI; 1998-086971/08.  
XX N-PSDB; AAV16524.  
XX  
XX New isolated *Bacillus thuringiensis* isolate(s) - used to obtain genes  
PT encoding toxins which are active against lepidopteran pests such as the  
PT Black cutworm.  
XX  
PS Claim 42; Page 131-133; 183pp; English.  
XX  
XX The present sequence represents a *Bacillus thuringiensis* toxin which is  
CC active against lepidopteran pests. The toxin isolates can be used for the  
CC control of lepidopteran pests such as *Agrotis ipsilon* (black cutworm),  
CC *Heliothis virescens* and *Helicoverpa zea*. PCR primers and probes can be  
CC derived from the polynucleotide encoding the toxin and used for the  
CC amplification and detection of other toxin-encoding sequences  
XX  
SQ Sequence 511 AA;  
  
Query Match 5.5%; Score 43; DB 2; Length 511;  
Best Local Similarity 100.0%; Pred. No. 4.2e-36;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 261 KTSSEVGNVNFILVLTALQAKAFLTTTCRKLGLADIDYT 303  
DB 122 KTSSEVGNVNFILVLTALQAKAFLTTTCRKLGLADIDYT 164  
  
RESULT 5  
AA124968  
ID AAY24968 standard; protein; 511 AA.  
XX  
AC AAY24968;  
XX  
DT 09-SEP-1999 (first entry)  
XX  
DE *Bacillus thuringiensis* toxin 94R1(a).  
XX  
XX *Bacillus thuringiensis*; toxin; *Ostrinia nubilalis*; lepidopteran;  
KM European corn borer; black cutworm.  
XX  
OS *Bacillus thuringiensis*.  
XX  
XX WO9333991-A2.  
PN  
PD 08-JUL-1999.  
XX  
PD 15-DEC-1998; 98WO-US026585.  
XX  
PR 31-DEC-1997; 97US-00002285.  
XX  
PA (MYCOG) MYCOGEN CORP.  
XX  
PI Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;  
PI Muller-Cohn J;  
XX  
XX WPI; 1999-405513/34.  
DR N-PSDB; AAX83885.  
XX  
XX Method for control of European corn borer using *Bacillus thuringiensis*  
PT toxins.  
XX  
XX Claim 1; Page 135-137; 174pp; English.  
XX  
XX A method has been developed for the control of European corn borer  
CC (*Ostrinia nubilalis*), comprising contacting the pest with a pesticidal  
CC amount of a *Bacillus thuringiensis* toxin. The method is used for the  
CC control of European corn borer (*Ostrinia nubilalis*). The method can also

CC be used for the control of other non-mammalian pests, particularly black  
CC cutworm, and other lepidopteran pests. The present sequence represents a  
CC *Bacillus thuringiensis* toxin from the present invention  
XX  
SQ Sequence 511 AA;  
  
Query Match 5.5%; Score 43; DB 2; Length 511;  
Best Local Similarity 100.0%; Pred. No. 4.2e-36;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 261 KTSSEVGNVNFILVLTALQAKAFLTTTCRKLGLADIDYT 303  
DB 122 KTSSEVGNVNFILVLTALQAKAFLTTTCRKLGLADIDYT 164  
  
RESULT 6  
AAW46864  
ID AAW46864 standard; protein; 759 AA.  
XX  
AC AAW46864;  
XX  
DT 11-JUN-1998 (first entry)  
XX  
XX *Bacillus thuringiensis* toxin designated 86W1(a).  
DE  
XX Toxin; lepidopteran pest; control; *Agrotis ipsilon*; black cutworm;  
KM *Heliothis virescens*; *Helicoverpa zea*.  
XX  
XX *Bacillus thuringiensis*.  
OS  
XX  
XX Key Location/Qualifiers  
FH  
FT Misc-difference 193  
FT  
FT /label= unknown  
FT /note= "encoded by AKT"  
FT /label= unknown  
FT /note= "encoded by AST"  
XX  
XX WO9800546-A2.  
PN  
XX  
XX 08-JAN-1998.  
PD  
XX  
XX 01-JUL-1997; 97WO-US011658.  
PF  
XX  
PR 01-JUL-1996; 96US-00674002.  
XX  
XX (MYCOG) MYCOGEN CORP.  
XX  
PI Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;  
PI  
XX  
XX WPI; 1998-086971/08.  
DR N-PSDB; AAV16523.  
XX  
XX New isolated *Bacillus thuringiensis* isolate(s) - used to obtain genes  
PT encoding toxins which are active against lepidopteran pests such as the  
PT Black cutworm.  
XX  
XX Claim 42; Page 126-129; 183pp; English.  
XX  
XX The present sequence represents a *Bacillus thuringiensis* toxin which is  
CC active against lepidopteran pests. The toxin isolates can be used for the  
CC control of lepidopteran pests such as *Agrotis ipsilon* (black cutworm),  
CC *Heliothis virescens* and *Helicoverpa zea*. PCR primers and probes can be  
CC derived from the polynucleotide encoding the toxin and used for the  
CC amplification and detection of other toxin-encoding sequences. note:  
CC nucleotide sequence contains numerous stop codons which do not alter the  
CC reading frame  
XX  
SQ Sequence 759 AA;  
  
Query Match 5.5%; Score 43; DB 2; Length 759;  
Best Local Similarity 100.0%; Pred. No. 6.1e-36;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      261 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 303
      |||
      262 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 304

Db

RESULT 7
AAY24967
AAY24967 standard; protein; 759 AA.
XX
AC      AAY24967;
XX
DT      09-SEP-1999 (first entry)
XX
DE      Bacillus thuringiensis toxin 86W1(a).
XX
KW      Bacillus thuringiensis; toxin; Ostrinia nubilalis; lepidopteran;
      European corn borer; black cutworm.
XX
OS      Bacillus thuringiensis.
XX
FH      Key Location/Qualifiers
FT      Misc-difference 193 /note= "unspecified"
FT      Misc-difference 257 /note= "unspecified"
XX
PN      WO9933991-A2.
XX
PD      08-JUL-1999.
XX
PF      15-DEC-1998; 98WO-US026585.
XX
PR      31-DEC-1997; 97US-00002285.
XX
PA      (MYCO ) MYCOGEN CORP.
XX
PI      Schnepf HE, Wäcker C, Narva KE, Walz M, Stockhoff BA;
      Müller-Cohn J;
XX
DR      WPI: 1999-405513/34.
      N-PSDB; AAX83884.
XX
PT      Method for control of European corn borer using Bacillus thuringiensis
      toxins.
XX
PS      Claim 1; Page 130-133; 174pp; English.
XX
CC      A method has been developed for the control of European corn borer
      (Ostrinia nubilalis), comprising contacting the pest with a pesticidal
      amount of a Bacillus thuringiensis toxin. The method is used for the
      control of European corn borer (Ostrinia nubilalis). The method can also
      be used for the control of other non-mammalian pests, particularly black
      cutworm, and other lepidopteran pests. The present sequence represents a
      Bacillus thuringiensis toxin from the present invention
XX
SQ      Sequence 759 AA;

Query Match      5.5%; Score 43; DB 2; Length 759;
Best Local Similarity 100.0%; Pred. No. 6.1e-36;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      261 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 303
      |||
      262 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 304

Db

RESULT 8
ADD43705
ADD43705 standard; protein; 786 AA.
XX
AC      ADD43705;
XX

```

```

DT      15-JAN-2004 (first entry)
XX
DE      Bacillus thuringiensis insecticidal protein ISPJ-2245J.
XX
KW      Insecticidal; plant insect pest; pesticide.
XX
OS      Bacillus thuringiensis.
XX
PN      WO2003080656-A1.
XX
PD      02-OCT-2003.
XX
PF      20-MAR-2003; 2003WO-EP003068.
XX
PR      22-MAR-2002; 2002US-0366276P.
XX
PR      06-NOV-2002; 2002US-0423999P.
XX
PA      (FARB ) BAYER BIOSCIENCE NV.
XX
PI      Arnaut G, Boets A, De Rudder K, Vanneste S, Van Rie J;
XX
DR      WPI; 2003-876903/81.
      N-PSDB; ADD43704.
XX
PT      New insecticidal proteins, useful for controlling plant insect pests, and
      for increasing resistance to insect damage compared to control plants.
XX
PS      Claim 2; SEQ ID NO 6; 81pp; English.
XX
CC      The present invention relates to Bacillus thuringiensis insecticidal
      proteins (ADD43701, ADD43703 and ADD43705) and their coding sequences
      (ADD43700, ADD43702 and ADD43704). The insecticidal proteins are
      CC      insecticidal against Helicoverpa zea, Helicoverpa virescens, Ostrinia
      CC      nubilalis, Spodoptera frugiperda, Agrotis ipsilon, Pectinophora
      CC      gossypiella, Scirphophaga incertulans, Chapulocrois medinalis, Sesamia
      CC      inferens, Chilo partellus and Anticarsia gemmatilis. The proteins are
      CC      useful for controlling plant insect pests, and for increasing resistance
      CC      to insect damage compared to control plants.
XX
SQ      Sequence 786 AA;

Query Match      5.5%; Score 43; DB 7; Length 786;
Best Local Similarity 100.0%; Pred. No. 6.3e-36;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      261 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 303
      |||
      262 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 304

Db

RESULT 9
ABB82567
ABB82567 standard; protein; 787 AA.
XX
AC      ABB82567;
XX
DT      04-FEB-2003 (first entry)
XX
DE      B. thuringiensis hybrid Vip3A-B toxin.
XX
KW      Vip3; toxin; insecticide; transgenic; delta-endotoxin; Vip3B; Vip3A.
XX
OS      Bacillus thuringiensis.
XX
PN      WO200278437-A2.
XX
PD      10-OCT-2002.
XX
PF      01-APR-2002; 2002WO-US010264.
XX
PR      30-MAR-2001; 2001US-0280025P.
XX
PR      04-DEC-2001; 2001US-033657P.
XX

```

PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX  
 PI Miles P, Kramer V, Shen Z, Shockoski F, Warren GW;  
 XX WPI: 2003-040603/03.  
 DR N-PSDB; ABV74980.  
 XX  
 PT Novel pesticidal toxin, designated Vip3 toxins from *Bacillus*  
 PT *thuringiensis*, useful for controlling insects, e.g., lepidopteran insect,  
 XX is highly active against a wide range of insect pests.  
 PS Example 9; Page 73-76; 82pp; English.  
 XX  
 CC The invention relates to an isolated Vip3 toxin from *B. thuringiensis*  
 CC that is active against insects. The toxins are useful for controlling  
 CC insects, where the insect is a lepidopteran insect selected from *Ostrinia*  
 CC *nubilalis* (European corn borer), *Plutella xylostella* (diamondback moth),  
 CC *Spodoptera frugiperda* (fall armyworm), *Agrotis ipsilon* (black cutworm),  
 CC *Helicoverpa zea* (corn earworm), *Heliothis virescens* (tobacco budworm), *S.*  
 CC *exigua* (beet armyworm), *Helicoverpa punctigera* (native budworm), *S.*  
 CC *Trichoplusia ni* (cabbage looper), *Pectinophora gossypiella* (pink  
 CC bollworm), and *Cochylis hospes* (banded sunflower moth). The  
 CC polynucleotides encoding the toxins are useful to produce an insect-  
 CC resistant transgenic plant. The toxins are useful in combination with Bt  
 CC delta-endotoxins to increase pest target range. The present sequence  
 CC represents a *B. thuringiensis* Vip3A-B hybrid toxin  
 XX  
 SQ Sequence 787 AA;  
 XX  
 Query Match 5.5%; Score 43; DB 6; Length 787;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-36;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 261 KTSGSEVGNVNNFLIVLTALQAKAFLLTTCRKLGLADIDYT 303  
 DB 262 KTSGSEVGNVNNFLIVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 10  
 ABB82565  
 ID ABB82565 standard; protein; 787 AA.  
 AC ABB82565;  
 XX  
 DT 04-FEB-2003 (first entry)  
 XX  
 DE *B. thuringiensis* native Vip3B polypeptide.  
 XX  
 KM Vip3; toxin; insecticide; transgenic; delta-endotoxin; Vip3B.  
 XX  
 OS *Bacillus thuringiensis*.  
 XX  
 PN WO200278437-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 01-APR-2002; 2002WO-US010264.  
 XX  
 PR 30-MAR-2001; 2001US-0280025P.  
 PR 04-DEC-2001; 2001US-0336657P.  
 XX  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX  
 PI Miles P, Kramer V, Shen Z, Shockoski F, Warren GW;  
 XX WPI: 2003-040603/03.  
 DR N-PSDB; ABV74977.  
 XX  
 PT Novel pesticidal toxin, designated Vip3 toxins from *Bacillus*  
 PT *thuringiensis*, useful for controlling insects, e.g., lepidopteran insect,  
 XX is highly active against a wide range of insect pests.  
 XX

PS Claim 4; Page 56-60; 82pp; English.  
 XX  
 CC The invention relates to an isolated Vip3 toxin from *B. thuringiensis*  
 CC that is active against insects. The toxins are useful for controlling  
 CC insects, where the insect is a lepidopteran insect selected from *Ostrinia*  
 CC *nubilalis* (European corn borer), *Plutella xylostella* (diamondback moth),  
 CC *Spodoptera frugiperda* (fall armyworm), *Agrotis ipsilon* (black cutworm),  
 CC *Helicoverpa zea* (corn earworm), *Heliothis virescens* (tobacco budworm), *S.*  
 CC *exigua* (beet armyworm), *Helicoverpa punctigera* (native budworm), *S.*  
 CC *Trichoplusia ni* (cabbage looper), *Pectinophora gossypiella* (pink  
 CC bollworm), and *Cochylis hospes* (banded sunflower moth). The  
 CC polynucleotides encoding the toxins are useful to produce an insect-  
 CC resistant transgenic plant. The toxins are useful in combination with Bt  
 CC delta-endotoxins to increase pest target range. The present sequence  
 CC represents a *B. thuringiensis* Vip3B toxin  
 XX  
 SQ Sequence 787 AA;  
 XX  
 Query Match 5.5%; Score 43; DB 6; Length 787;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-36;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 261 KTSGSEVGNVNNFLIVLTALQAKAFLLTTCRKLGLADIDYT 303  
 DB 262 KTSGSEVGNVNNFLIVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 11  
 ADN08758  
 ID ADN08758 standard; protein; 787 AA.  
 XX  
 AC ADN08758;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE *B. thuringiensis* Vip3B protein SEQ ID NO:7.  
 XX  
 KM Vip3C; toxin; protease inhibitor; lepidopteran; tobacco budworm;  
 KM sunflower head moth; beet armyworm; insect-resistance; maize; Vip3B.  
 XX  
 OS *Bacillus thuringiensis*.  
 XX  
 PN WO2003075655-A2.  
 XX  
 PD 18-SEP-2003.  
 XX  
 PF 20-FEB-2003; 2003WO-US004735.  
 XX  
 PR 06-MAR-2002; 2002US-0362250P.  
 XX  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX  
 PI Shen Z, Warren GW, Shockoski F, Kramer V;  
 XX WPI: 2003-788166/74.  
 DR N-PSDB; ADN08757.  
 XX  
 PT New Vip3 toxin encoded by a nucleic acid from *Bacillus thuringiensis*,  
 PT useful for controlling lepidopteran insects such as tobacco budworm,  
 PT sunflower head moth or beet armyworm, or for producing an insect-  
 PT resistant transgenic plant.  
 XX  
 PS Example 10; SEQ ID NO 7; 118pp; English.  
 XX  
 CC The invention relates to a novel isolated Vip3 toxin that is active  
 CC against insects. The toxin acts as a protease inhibitor. The Vip3 toxin,  
 CC hybrid toxin and nucleic acid molecules are useful for controlling  
 CC lepidopteran insects such as tobacco budworm, sunflower head moth or beet  
 CC armyworm, for producing an insect-resistant transgenic plant, and  
 CC protecting a maize plant against at least one insect pest. The present  
 CC sequence represents native *B. thuringiensis* Vip3B.  
 XX



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XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX PI Shen Z, Warren GW, Shokoski F, Kramer V;
XX WPI; 2003-788166/74.
XX DR N-PSDB; ADN08761.
XX
XX PT New Vip3 toxin encoded by a nucleic acid from Bacillus thuringiensis,
XX PT useful for controlling lepidopteran insects such as tobacco budworm,
XX PT sunflower head moth or beet armyworm, or for producing an insect-
XX PT resistant transgenic plant.
XX
XX PS Claim 12; SEQ ID NO 11, 118pp; English.
XX
XX CC The invention relates to a novel isolated Vip3 toxin that is active
XX CC against insects. The toxin acts as a protease inhibitor. The Vip3 toxin,
XX CC hybrid toxin and nucleic acid molecules are useful for controlling
XX CC lepidopteran insects such as tobacco budworm, sunflower head moth or beet
XX CC armyworm, for producing an insect-resistant transgenic plant, and
XX CC protecting a maize plant against at least one insect pest. The present
XX CC sequence represents vip3A-C, a B. thuringiensis vip3A-vip3C fusion
XX CC protein.
XX
XX SQ Sequence 788 AA;

Query Match          5.5%; Score 43; DB 7; Length 788;
Best Local Similarity 100.0%; Pred. No. 6.3e-36;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEVGNVYNNFLIVLTALQAKAFLTTTCRKLLGLADIDYT 303
Db 262 KTSGSEVGNVYNNFLIVLTALQAKAFLTTTCRKLLGLADIDYT 304

RESULT 15
AAW60216
ID AAW60216 standard; protein; 789 AA.
XX
XX AC AAW60216;
XX
XX DT 17-OCT-2003 (revised)
XX DT 28-SEP-1998 (first entry)
XX
XX DE Bacillus thuringiensis insecticidal 81F toxin.
XX
XX KW Insecticide; pesticide; toxin; biological control; lepidopteran;
XX KW coleopteran.
XX
XX OS Bacillus thuringiensis; strain PS81F (NRRL B-18424).
XX
XX PN MO9818932-A2.
XX
XX PD 07-MAY-1998.
XX
XX PF 30-OCT-1997; 97MO-US019804.
XX
XX PR 30-OCT-1996; 96US-0029848P.
XX
XX PA (MYCO ) MYCOGEN CORP.
XX
XX PI Feltelson JS, Schepf HR, Narva KE, Stockhoff BA, Schmeits JL,
XX PI Loewer D, Schwab G, Dullum CJ, Muller-Cohn J, Stamp L;
XX DR WPI; 1998-272226/24.
XX DR N-PSDB; AAV30289.
XX
XX PT Bacillus thuringiensis isolates - used for producing pesticidal toxins
XX PT and nucleotide sequences for control of lepidopterans and coleopterans.
XX
XX PS Example 4; Page 51-53; 139pp; English.
XX
XX CC This polypeptide comprises the novel 81F toxin of isolate PS81F of

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CC Bacillus thuringiensis (B.t.). Its amino acid sequence was deduced from
CC DNA (see AAV30289) isolated by PCR amplification following
CC identification of PS81F as a producer of lepidopteran-active toxin.
CC Disclosed and claimed are novel B.t. isolates, pesticidal toxins (see
CC AAW60215-32), genes and nucleotide probes and primers (see AAV30288-321
CC and AAV99734-87) for the identification of genes encoding toxins active
CC against pests, and transformed host cells. The invention provides
CC entirely new families of toxins from Bacillus isolates. (Updated on 17-
CC OCT-2003 to standardise OS field)
XX
XX SQ Sequence 789 AA;

Query Match          5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 6.3e-36;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEVGNVYNNFLIVLTALQAKAFLTTTCRKLLGLADIDYT 303
Db 262 KTSGSEVGNVYNNFLIVLTALQAKAFLTTTCRKLLGLADIDYT 304

Search completed: May 15, 2006, 20:51:37
Job time : 189 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using bw model

Run on: May 15, 2006, 20:51:56 ; Search time 44 Seconds  
(without alignments)  
1718.781 Million cell updates/sec

Title: US-10-698-096-17

Perfect score: 786

Sequence: 1 MQKNKLKSVKALPSFIDYFN.....VELSRASRGVINFDFSIR 786

Scoring table: OLIGO  
Gapop 60.0 , Gapept 60.0

Searched: 283416 seqs, 96216763 residues

Worf 8329 8 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR-80.\*

1: p1r1.\*  
2: p1r2.\*  
3: p1r3.\*  
4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	1.1	595	2 B97866	DNA primase (EC 2.7.7.7) [imported] - Rickettsia conorii (strain Malish 7)
2	9	1.1	621	2 T11976	glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) [similarity]
3	9	1.1	1381	1 S45781	probable calcium-b
4	8	1.0	125	2 A86789	hypothetical prote
5	8	1.0	136	2 C71328	probable flagellar
6	8	1.0	152	2 A97003	probable beta-D-ga
7	8	1.0	250	2 S56156	Rieske iron-sulfur
8	8	1.0	308	2 S44818	P44E2.8 protein -
9	8	1.0	359	2 A70978	probable rmlA2 pro
10	8	1.0	418	2 B86871	protease (import
11	8	1.0	420	2 S51492	48-7k intron prote
12	8	1.0	448	2 S50622	hypothetical prote
13	8	1.0	461	2 H81319	probable ADP-hept
14	8	1.0	495	2 H84359	threonine dehydrat
15	8	1.0	689	2 B69135	coenzyme F420-redu
16	8	1.0	795	2 AE0705	phenylalanyl-tRNA
17	8	1.0	1252	2 T14272	phenylalanyl-tRNA
18	8	1.0	66	2 T28235	ORF MSV073 hypoch
19	7	0.9	83	2 J05745	coronafacic acid s
20	7	0.9	111	2 S03304	ig kappa chain V r
21	7	0.9	113	2 C90083	hypothetical prote
22	7	0.9	114	2 B87339	conserved hypochet
23	7	0.9	132	2 H72632	hypothetical prote
24	7	0.9	133	2 B69279	conserved hypochet
25	7	0.9	135	2 T02391	hypothetical prote
26	7	0.9	136	2 H82787	hypothetical prote
27	7	0.9	139	2 T49650	hypothetical prote
28	7	0.9	144	2 T01823	hypothetical prote
29	7	0.9	156	1 R3XT7	ribosomal protein

30	7	0.9	158	2 G90332	hypothetical prote
31	7	0.9	168	2 B69776	hypothetical prote
32	7	0.9	176	2 F72430	MAP-reducing hydr
33	7	0.9	184	2 F89839	ribosome recycling
34	7	0.9	189	2 G84451	probable cold-regu
35	7	0.9	193	2 H84958	phosphoprotease iso
36	7	0.9	193	2 AH2372	hypothetical prote
37	7	0.9	195	2 AE2755	conserved hypochet
38	7	0.9	198	2 C82357	transcription regu
39	7	0.9	209	2 H69901	general stress pro
40	7	0.9	215	2 E96533	hypothetical prote
41	7	0.9	218	2 D97536	hypothetical prote
42	7	0.9	229	2 JC7308	cellulase (EC 3.2.2)
43	7	0.9	231	2 D87715	carboxymethylendu
44	7	0.9	237	2 A84957	N-acetylmutamoyl-L
45	7	0.9	239	2 AE0772	probable exported

#### ALIGNMENTS

RESULT 1  
B97866  
DNA primase (EC 2.7.7.7) [imported] - Rickettsia conorii (strain Malish 7)  
C:Species: Rickettsia conorii  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: B97866  
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; f  
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A:Reference number: A97700; MUID:21442074; PMID:11557893  
A:Accession: B97866  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-595 <KUR>  
A:Cross-references: UNIPROT:Q92FZ7; UNIPARC:UPI00000CC08A; GB:AE006914; PIDN:AAL03868.1  
A:Genetics:  
A:Gene: dnaG  
A:Superfamily: DNA primase  
C:Keywords: nucleotidyltransferase  
Query Match 1.1% Score 9; DB 2; Length 595;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 86 KEIKIANE 94  
Db 573 KEIKIANE 581  
RESULT 2  
T11976  
glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) [similarity] -  
C:Species: chloroplast Cyanidium caldarium  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: T11976  
R:Goeckner, G.; Rosenthal, A.; Valentin, K.  
A:Submitted to the EMBL Data Library, September 1997  
A:Description: Organisation of 46 kb of the Cyanidium caldarium RK1 plastid genome.  
A:Reference number: 217374  
A:Accession: T11976  
A:Status: preliminary; translated from GB/EMBL/DBD  
A:Molecule type: DNA  
A:Residues: 1-621 <GLO>  
A:Cross-references: UNIPROT:O19908; UNIPARC:UPI0000163753; EMBL:AF022186; NID:g2465730;  
A:Experimental source: strain RK1  
C:Genetics:  
A:Gene: chlroplast  
A:Note: gcaA  
C:Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)  
C:Keywords: aminotransferase; chloroplast; isomerase  
F:2-621/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status pred  
F:2/Active site: Cys #status predicted

Query Match 1.1%; Score 9; DB 2; Length 621;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 LSKOLKEIS 149  
DB 470 LSKOLKEIS 478

RESULT 3  
S45781  
probable calcium-binding protein YBL047C - yeast (Saccharomyces cerevisiae)  
N/Alternate names: hypothetical protein YBL0520  
C/Species: Saccharomyces cerevisiae  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: S45781; S50284; S45782; S39841; S37339; S42398  
R/Goffeau, A.; Jonniaux, J.L.; Purnelle, B.; Skala, J.; de Wergifosse, P.; van Dyck, L.  
submitted to the Protein Sequence Database, August 1994  
A/Reference number: S45745  
A/Accession: S45781  
A/Molecule type: DNA  
A/Residues: 1-961 <COF>  
A/Cross-references: UNIPROT:P34216; UNIPARC:UPI0000174C49; EMBL:Z35808; GSPDB:GNO0002; N  
A/Experimental source: strain S288C  
R/de Wergifosse, P.; Jacques, B.; Jonniaux, J.L.; Purnelle, B.; Skala, J.; Goffeau, A.  
Yeast 10, 1489-1496, 1994  
A/Title: The sequence of a 22.4 kb DNA fragment from the left arm of yeast chromosome II  
NA-binding protein.  
A/Reference number: S50284; MUID:95176707; PMID:7871888  
A/Accession: S50284  
A/Molecule type: DNA  
A/Residues: 1-961 <DEF>  
A/Cross-references: UNIPARC:UPI0000174C49; EMBL:X78214  
R/Dubois, E.; El Bakoury, M.; Glansdorff, N.; Messenguy, F.; Pierard, A.; Scherens, B.;  
submitted to the Protein Sequence Database, August 1994  
A/Reference number: S45782  
A/Accession: S45782  
A/Molecule type: DNA  
A/Residues: 579-1381 <DOB>  
A/Cross-references: UNIPARC:UPI0000168C7F; EMBL:Z35808; GSPDB:GNO0002; MIPS:YBL047C  
R/Scherens, B.; el Bakoury, M.; Vlerendael, F.; Dubois, E.; Messenguy, F.  
Yeast 9, 1355-1371, 1993  
A/Title: Sequencing and functional analysis of a 32 560 bp segment on the left arm of ye  
A/Reference number: S39824; MUID:94205266; PMID:8154187  
A/Accession: S39841  
A/Molecule type: DNA  
A/Residues: 579-1381 <SCH>  
A/Cross-references: UNIPARC:UPI0000168C7F; EMBL:Z23261; NID:G313733; PIDN:CAA80797.1; PI  
A/Experimental source: strain S288C  
C/Genetics:  
A/Gene: SGD:EDL1; MIPS:YBL047C  
A/Cross-references: SGD:S0000143  
A/Map position: 2L  
C/Superfamily: Yeast probable calcium-binding protein YBL047C; calmodulin repeat homolog  
C/Keywords: calcium binding; EF hand; transmembrane protein  
F.167-199/Domain: calmodulin repeat homology <EF1>  
F.560-576/Domain: transmembrane #status predicted <TM>

Query Match 1.1%; Score 9; DB 1; Length 1381;  
Best Local Similarity 100.0%; Pred. No. 5;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 NSINDLLA 76  
DB 421 NSINDLLA 429

RESULT 4  
A86789  
hypothetical protein yneH [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C/Species: Lactococcus lactis subsp. lactis  
C/Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C/Accession: A86789  
R/Bolotin, A.; Wincer, P.; Mauger, S.; Jalllon, O.; Malarme, K.; Weisenbach, J.; Ehrh  
Genome Res. 11, 731-753, 2001  
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s  
A/Reference number: A86625; MUID:21235186; PMID:11337471  
A/Accession: A86789  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-125 <STO>  
A/Cross-references: UNIPROT:Q9CFZ8; UNIPARC:UPI000006A07; GB:AE005176; PID:G12724292; I  
A/Experimental source: strain IL1403  
C/Genetics:  
A/Gene: yneH

Query Match 1.0%; Score 8; DB 2; Length 125;  
Best Local Similarity 100.0%; Pred. No. 5.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 ILKNQOLL 57  
DB 89 ILKNQOLL 96

RESULT 5  
C71328  
probable flagellar basal-body rod protein (flgB) - syphilis spirochete  
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C/Accession: C71328  
R/Frazer, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwif  
erson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McCo  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998  
A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A/Reference number: A71250; MUID:98332770; PMID:965876  
A/Accession: C71328  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-136 <COL>  
A/Cross-references: UNIPROT:O83411; UNIPARC:UPI00000D3249; GB:AE001218; GB:AE000520; NIT  
A/Experimental source: strain Nichols  
C/Genetics:  
A/Gene: TP0396  
C/Superfamily: rod protein flgB

Query Match 1.0%; Score 8; DB 2; Length 136;  
Best Local Similarity 100.0%; Pred. No. 6.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 433 LRYEVTAN 440  
DB 20 LRYEVTAN 27

RESULT 6  
A97003  
probable beta-D-galactosidase [imported] - Clostridium acetobutylicum  
C/Species: Clostridium acetobutylicum  
C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: A97003  
R/Nolling, U.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
A/Reference number: A96900; MUID:21359325; PMID:21359325  
A/Accession: A97003  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-152 <KUR>  
A/Cross-references: UNIPROT:Q97KTO; UNIPARC:UPI00000C9PD0; GB:AE001437; PIDN:AAK78812.1,  
A/Experimental source: Clostridium acetobutylicum ATCC824



C:Genetics:  
A:Gene: CAC0836

Query Match 1.0%; Score 8; DB 2; Length 152;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 596 IQYIVKGR 603  
|||  
Db 72 IQYIVKGR 79

## RESULT 7

S56156  
Rieske iron-sulfur protein soxP - Sulfolobus acidocaldarius  
N:Alternate names: Rieske iron-sulfur protein II  
C:Species: Sulfolobus acidocaldarius  
C>Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S56156; S56173  
R:Castresana, J.; Luebben, M.; Saraste, M.  
J. Mol. Biol. 250, 202-210, 1995  
A:Title: New archaebacterial genes coding for redox proteins: implications for the evolution of the iron-sulfur cluster  
A:Reference number: S56155; MUID:95333177; PMID:7608970  
A:Accession: S56156  
A:Status: nucleic acid sequence not shown  
A:Residues: 1-250 <CAS>  
A:Molecule type: DNA  
A:Cross-references: UNIPROT:Q53766; UNIPARC:UPI0000062706; EMBL:Z48338; NID:9927521; PIR:J01401

A:Accession: S56173  
A:Molecule type: protein  
A:Residues: 1-24 <CAZ>  
A:Cross-references: UNIPARC:UPI000017A86  
C:Species: Caenorhabditis elegans  
C:Keywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein  
F:130-190/Domin: Rieske [2Fe-2S] homology #status atypical <RSK>  
F:140,142,170,173/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status p

Query Match 1.0%; Score 8; DB 2; Length 250;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 YDSSTGDI 449  
|||  
Db 201 YDSSTGDI 208

## RESULT 8

S44818  
F44B2.8 protein - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S44818  
R:Anderson, K.

submitted to the EMBL Data Library, September 1993  
A:Description: Sequence of the C. elegans cosmid F44B2.  
A:Reference number: S44816  
A:Accession: S44818  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1308 <AND>

A:Cross-references: UNIPROT:P34438; UNIPARC:UPI000013B7D5; EMBL:L23646; NID:9388595; PIR:J01401  
C:Genetics:  
A:introns: 37/3; 103/3; 242/2

Query Match 1.0%; Score 8; DB 2; Length 308;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 363 KDSIAVLK 370  
|||  
Db 204 KDSIAVLK 211

## RESULT 9

A70978  
probable rmlA2 protein - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: A70978

R:Coile, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, J.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Suleron, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: A70978  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-359 <COL>  
A:Cross-references: UNIPROT:P96869; UNIPARC:UPI000005ECC; GB:Z92771; GB:AL123456; NID:J01401

A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: rmlA2  
C:Superfamily: mannose-1-phosphate guanylyltransferase

Query Match 1.0%; Score 8; DB 2; Length 359;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 ALGQITRY 140  
|||  
Db 74 ALGQITRY 81

## RESULT 10

E86871  
Proteinase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
C:Species: Lactococcus lactis subsp. lactis  
C>Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: E86871

R:Bohlool, A.; Winkler, P.; Manger, S.; Jallion, O.; Malarme, K.; Weisenbach, J.; Ehrlich, G. Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: E86871  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-418 <STO>

A:Cross-references: UNIPROT:Q9CE72; UNIPARC:UPI000006B77; GB:AE005176; PIR:G12725016;  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: yuef

Query Match 1.0%; Score 8; DB 2; Length 418;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 SEIJAEN 259  
|||  
Db 163 SEIJAEN 170

## RESULT 11

S51492  
48.7K intron protein - fungus (Sclerotinia sclerotiorum) mitochondrion  
C:Species: mitochondrion Sclerotinia sclerotiorum  
C>Date: 19-Mar-1997 #sequence\_revision 09-May-1997 #text\_change 09-Jul-2004  
C:Accession: S51492

R:Carbone, I.; Anderson, J.B.; Kohn, L.M. Curr. Genet. 27, 166-176, 1995  
A:Title: A group-I intron in the mitochondrial small subunit ribosomal RNA gene of Scler  
A:Reference number: S51492; MUID:95308539; PMID:7788720  
A:Accession: S51492  
A:Molecule type: DNA  
A:Residues: 1-420 <CAR>  
A:Cross-references: UNIPROT:Q35928; UNIPARC:UPI0000097183; EMBL:U07553; NID:9466463; PIR:J01401

A:Experimental source: host Brassica napus  
C:Genetics:  
A:Genome: mitochondrion  
A:Genetic code: SGC3  
C:Keywords: mitochondrion

Query Match 1.0%; Score 8; DB 2; Length 420;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 MNEHLNKE 313  
|||||  
Db 241 MNEHLNKE 248

## RESULT 12

S50622  
Hypothetical protein YER119c - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 28-May-1993 #sequence\_revision 24-Feb-1995 #text\_change 09-Jul-2004

C:Accession: S50622; S57257

R:Dieterich, F.S.

submitted to the EMBL Data Library, December 1994

A:Description: The sequence of S. cerevisiae cosmids 9781, 8198, 9115, 9981, and lambda

A:Reference number: S50437

A:Accession: S50622

A:Molecule type: DNA

A:Residues: 1-448 <DIE>

A:Cross-references: UNIPROT:P40074; UNIPARC:UPI000013ACBF; EMBL:U18916; NID:G1384128; PI

R:Berroteran, R.W.; Hampsey, M.

Yeast 11, 761-766, 1995

A:Title: Sequence, map position and genome organization of the RPL17B gene, encoding rib

A:Reference number: S57256; MUID:9537553; PMID:7668045

A:Accession: S57257

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 270-448 <BER>

A:Cross-references: UNIPARC:UPI00001689F3; EMBL:U15653; NID:G642467; PIDD:AAA61905.1; PI

C:Genetics:

A:Map position: 5R

C:Superfamily: Saccharomyces cerevisiae probable membrane protein YBL089w

## Query Match

1.0%; Score 8; DB 2; Length 448;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 KKLNSLR 435  
|||||  
Db 141 KKLNSLR 148

## RESULT 13

H81319  
probable ADP-heptose synthase Cj1150c [imported] - Campylobacter jejuni (strain NCTC 111

C:Species: Campylobacter jejuni

C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C:Accession: H81319

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyf

A:Reference number: A81250; MUID:20150912; PMID:10688204

A:Accession: H81319

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-461 <PAR>

A:Cross-references: UNIPROT:Q9PNB5; UNIPARC:UPI00000C1E38; GB:AL139077; GB:AL111168; NID

C:Genetics:

A:Gene: waab; Cj1150c

C:Superfamily: hypothetical protein b3052

Query Match 1.0%; Score 8; DB 2; Length 461;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 542 NIEGENTLE 549  
|||||  
Db 203 NIEGENTLE 210

## RESULT 14

H84359  
Threonine dehydratase [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C:Accession: H84359

R:Ng, W.V.; Kennedy, S.P.; Mahapatra, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.

; Leitbauer, B.; Keller, K.; Cruz, R.; Dawson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabic

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebdhardt, H.; Lowe, T.M.; Li

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: H84359

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-495 <STO>

A:Cross-references: UNIPROT:Q9HNM6; UNIPARC:UPI0000063A49; GB:AE004437; NID:G10581515; E

C:Genetics:

A:Gene: tluA

Query Match 1.0%; Score 8; DB 2; Length 495;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 GSLINDILA 76  
|||||  
Db 423 GSLINDILA 430

## RESULT 15

E69135  
coenzyme F420-reducing hydrogenase, beta subunit homolog - Methanobacterium thermoautotr

C:Species: Methanobacterium thermoautotrophicum

C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 05-Oct-2004

C:Accession: E69135

R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N

ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct

A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Accession: E69135

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-689 <MTH>

A:Cross-references: UNIPROT:Q26380; UNIPARC:UPI0000066710; GB:AE000813; GB:AE000666; NID

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH280

F/18-132/Domain: ferredoxin 2[4Fe-4S] homology <FER>

Query Match 1.0%; Score 8; DB 2; Length 689;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 ALKTASEL 254  
|||||  
Db 211 ALKTASEL 218

Search completed: May 15, 2006, 20:56:25  
Job time : 46 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 20:48:41 ; Search time 232 Seconds  
(without alignments)  
2390.281 Million cell updates/sec

Title: US-10-698-096-17  
Perfect score: 786  
Sequence: 1 MOKNNKLXVXALPSPIDYFN.....VELSRASSRGVINFDPFSIK 786

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	5.9	787	2	Q5JZY8_BACTU
2	43	5.5	166	2	Q93D76_BACTU
3	43	5.5	190	2	Q93D74_BACTU
4	43	5.5	786	2	Q5JZY9_BACTU
5	43	5.5	788	2	Q5JZY0_BACTU
6	43	5.5	789	2	Q5JZY1_BACTU
7	43	5.5	789	2	Q5JZY2_BACTU
8	43	5.5	789	2	Q5JZY3_BACTU
9	43	5.5	789	2	Q5JZY4_BACTU
10	43	5.5	789	2	Q5JZY5_BACTU
11	43	5.5	789	2	Q5JZY6_BACTU
12	43	5.5	789	2	Q5JZY7_BACTU
13	43	5.5	789	2	Q5JZY8_BACTU
14	43	5.5	789	2	Q5JZY9_BACTU
15	43	5.5	789	2	Q5JZY0_BACTU
16	43	5.5	789	2	Q5JZY1_BACTU
17	43	5.5	789	2	Q5JZY2_BACTU
18	43	5.5	789	2	Q5JZY3_BACTU
19	43	5.5	789	2	Q5JZY4_BACTU
20	43	5.5	789	2	Q5JZY5_BACTU
21	43	5.5	789	2	Q5JZY6_BACTU
22	43	5.5	789	2	Q5JZY7_BACTU
23	43	5.5	789	2	Q5JZY8_BACTU
24	43	5.5	789	2	Q5JZY9_BACTU
25	43	5.5	789	2	Q5JZY0_BACTU
26	43	5.5	789	2	Q5JZY1_BACTU
27	43	5.5	789	2	Q5JZY2_BACTU
28	43	5.5	789	2	Q5JZY3_BACTU
29	43	5.5	789	2	Q5JZY4_BACTU
30	43	5.5	789	2	Q5JZY5_BACTU
31	43	5.5	789	2	Q5JZY6_BACTU

32	9	1.1	1381	1	YBE7_YEAST	P34216 saccharomyc
33	9	1.1	1803	2	Q4Q678_LEIMA	Q4Q678 leishmania
34	9	1.1	3753	2	Q846W6_STRCM	Q846W6 streptomyc
35	8	1.0	94	2	Q722A3_LISMF	Q722A3 listeria mo
36	8	1.0	111	2	Q9K5C4_CORGL	Q9K5C4 corynebacte
37	8	1.0	111	2	Q9LAK8_CORGL	Q9LAK8 corynebacte
38	8	1.0	125	2	Q9CFZ8_LACLA	Q9CFZ8 lactococcu
39	8	1.0	130	2	Q4HG95_CAMCO	Q4HG95 campylobact
40	8	1.0	136	2	Q83411_TREPA	Q83411 treponema p
41	8	1.0	149	2	Q701X6_PCREN	Q701X6 uncultured
42	8	1.0	152	2	Q97KT0_CLOAB	Q97KT0 clostridium
43	8	1.0	239	2	Q50154_STRBO	Q50154 streptococc
44	8	1.0	242	1	Y158_CABEL	P34438 caenorhabdi
45	8	1.0	250	2	Q53766_SULAC	Q53766 sulfolobus

#### ALIGNMENTS

RESULT 1  
ID Q5JZY8\_BACTU PRELIMINARY; PRT; 787 AA.  
AC Q5JZY8;  
DT 10-MAY-2005 (TREMBlrel. 30, Created)  
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
DE Isp3c protein.  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Van Rie J., Arnaut G., Boets A., Damme N.;  
RT "Gene encoding insecticidal secreted proteins from Bacillus thuringiensis."  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ872072; CAI43277.1; -; Genomic DNA.  
DR GO: GO:0016798; P:hydrolase activity, acting on glycosyl bonds; IEA.  
DR GO: GO:0016491; P:oxidoreductase activity; IEA.  
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro: IPR003305; CBM Cenc.  
DR Pfam: PF02018; CBM\_4\_9; I.  
KW Oxidoreductase.  
SQ SEQUENCE 787 AA; 88359 MW; 0B1AF7876FF30D62 CRC64;  
Query Match 5.9%; Score 46; DB 2; Length 787;  
Best Local Similarity 100.0%; Pred. No. 2e-37;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 514 LLAIDLSNKKETKLVPPNGFISNIIVENGNIENGLFEPWKANNQAY 559  
Db 515 LLAIDLSNKKETKLVPPNGFISNIIVENGNIENGLFEPWKANNQAY 560  
RESULT 2  
ID Q93D76\_BACTU PRELIMINARY; PRT; 166 AA.  
AC Q93D76;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Insecticidal protein Vip3A (fragment).  
GN Name=Vip3A;  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Loguercio L.L., Barreto M.R., Rocha T.L., Lana U.G.P., Paiva E.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

```

RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=474L;
RA Loguercio L.L., Barreto M.R., Rocha T.L., Santos C.G., Teixeira F.F.,
  Paiva E.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF399670; AAK97485.1; -; Genomic_DNA.
FT NON_TER 1
  1
FT NON_TER 166
  166
SQ SEQUENCE 166 AA; 18517 MW; D76BDAB1C2E9F170 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 2; Length 166;
Pred. No. 6.4e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVNFLLVLTALQAKAFLLTTCRKLGLADIDYT 303
  |||
DB 55 KTSGEVGNVNFLLVLTALQAKAFLLTTCRKLGLADIDYT 97

```

```

RESULT 3
Q93D74 BACTU
ID Q93D74_BACTU PRELIMINARY; PRT; 190 AA.
AC Q93D74;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE Insecticidal protein Vip3A (Fragment).
GN Name=vip3A;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
  [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1165A;
RA Loguercio L.L., Barreto M.R., Rocha T.L., Lana U.G.P., Paiva E.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
  [2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=1165A;
RA Loguercio L.L., Barreto M.R., Rocha T.L., Santos C.G., Teixeira F.F.,
  Paiva E.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF399673; AAK97487.1; -; Genomic_DNA.
FT NON_TER 1
  1
FT NON_TER 190
  190
SQ SEQUENCE 190 AA; 21007 MW; 2D7D9377CE3647B1 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 2; Length 190;
Pred. No. 7.2e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVNFLLVLTALQAKAFLLTTCRKLGLADIDYT 303
  |||
DB 68 KTSGEVGNVNFLLVLTALQAKAFLLTTCRKLGLADIDYT 110

```

```

RESULT 4
Q5JZV9 BACTU
ID Q5JZV9_BACTU PRELIMINARY; PRT; 786 AA.
AC Q5JZV9;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Iap3b protein.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
  [1]
RN NUCLEOTIDE SEQUENCE.
RP Van Rie J., Arnaut G., Boets A., Damme N.;

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RT "Genes encoding insecticidal secreted proteins from Bacillus
  thuringiensis."
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ872071; CA143276.1; -; Genomic_DNA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR003305; CBM_Cenc.
DR Pfam; PF02018; CBM_4_9; I.
KM Oxidoreductase.
SQ SEQUENCE 786 AA; 88997 MW; B67FD67CBA56A57 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 2; Length 786;
Pred. No. 2.4e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVNFLLVLTALQAKAFLLTTCRKLGLADIDYT 303
  |||
DB 262 KTSGEVGNVNFLLVLTALQAKAFLLTTCRKLGLADIDYT 304

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RESULT 5
Q5JZV9 BACTU
ID Q5JZV9_BACTU PRELIMINARY; PRT; 788 AA.
AC Q5JZV9;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Iap3a protein.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
  [1]
RP NUCLEOTIDE SEQUENCE.
RA Van Rie J., Arnaut G., Boets A., Damme N.;
RT "Genes encoding insecticidal secreted proteins from Bacillus
  thuringiensis."
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ872070; CA143275.1; -; Genomic_DNA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR003305; CBM_Cenc.
DR Pfam; PF02018; CBM_4_9; I.
KM Oxidoreductase.
SQ SEQUENCE 788 AA; 88037 MW; 5A7314A1DA4A60B8 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 2; Length 788;
Pred. No. 2.4e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVNFLLVLTALQAKAFLLTTCRKLGLADIDYT 303
  |||
DB 262 KTSGEVGNVNFLLVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 6
Q69270 BACTU
ID Q69270_BACTU PRELIMINARY; PRT; 789 AA.
AC Q69270;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Vegetative insecticidal protein.
GN Name=vip-s;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
  [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=A13; TISSUE=Leaf;

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RX MEDLINE=21579339; PubMed=11722946;
RI DOI=10.1128/AEM.67.12.5855-5858.2001;
RA Selvapandian A., Arora N., Rajagopal R., Jalali S.K., Venkatesan T.,
RA Singh S.P., Bhattacharjee R.K.;
RT "Toxicity analysis of N- and C-terminus-deleted vegetative
RT insecticidal protein from Bacillus thuringiensis.";
RL Appl. Environ. Microbiol. 67:5855-5858(2001).
DR EMBL; Y17158; CAA76665.1; -; Genomic DNA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR003305; CBM_Cenc.
DR Pfam; PF02018; CBM_4_9; 1.
KM Oxidoreductase.
SQ SEQUENCE 789 AA; 88599 MW; 70619EAB6823C7AC CRC64;

Query Match 5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 261 KTSGEVGNVNFLLIVLTALQAKAFLLTTCRKLGLADIDYT 303
Db 262 KTSGEVGNVNFLLIVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 7
Q8XP05_BACTU
ID Q8XP05_BACTU PRELIMINARY; PRT; 789 AA.
AC Q8XP05;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Vip3A.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NY-197;
RA Li J., Yan J., Yuan Z.;
RT "Cloning and expression of vip3A gene from Bacillus thuringiensis
RT strain NY-197.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY743436; AAU89707.1; -; Genomic DNA.
DR GO; GO:0016798; F:hydrolase activity; acting on glycosyl bonds; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR003305; CBM_Cenc.
DR Pfam; PF02018; CBM_4_9; 1.
KM Oxidoreductase.
SQ SEQUENCE 789 AA; 88642 MW; 6322FDA4A8BC70D4 CRC64;

Query Match 5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 261 KTSGEVGNVNFLLIVLTALQAKAFLLTTCRKLGLADIDYT 303
Db 262 KTSGEVGNVNFLLIVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 8
Q79SG2_BACTU
ID Q79SG2_BACTU PRELIMINARY; PRT; 789 AA.
AC Q79SG2;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Vegetative insecticidal protein.
GN Name=Vi83;
OS Bacillus thuringiensis serovar lewisii.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=169759;

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=YBT-833;
RA Cai Q., Liu Z., Sun M., Yu Z.;
RT "Vegetative insecticidal protein gene vip83 from Bacillus
RT thuringiensis serovar lewisii strain YBT-833.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY044227; AAK95326.1; -; Genomic DNA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR003305; CBM_Cenc.
DR Pfam; PF02018; CBM_4_9; 1.
KM Oxidoreductase.
SQ SEQUENCE 789 AA; 88671 MW; 9DD746486823C7AB CRC64;

Query Match 5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 261 KTSGEVGNVNFLLIVLTALQAKAFLLTTCRKLGLADIDYT 303
Db 262 KTSGEVGNVNFLLIVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 9
Q8RSZ5_BACTU
ID Q8RSZ5_BACTU PRELIMINARY; PRT; 789 AA.
AC Q8RSZ5;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Vip3A (Vip184).
GN Name=Vip3A;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SI84;
RX MEDLINE=22744951; PubMed=12859763;
RX DOI=10.1046/j.1365-2672.2003.01977.x;
RA Chen J., Yu J., Tang L., Tang M., Shi Y., Pang Y.;
RT "Comparison of the expression of Bacillus thuringiensis full-length
RT and N-terminally truncated vip3A gene in Escherichia coli.";
RL J. Appl. Microbiol. 95:310-316(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SI84;
RX PubMed=12674638;
RA Chen J.W., Tang L.X., Tang M.J., Shi Y.X., Pang Y.;
RT "[Cloning and expression product of vip3A gene from Bacillus
RT thuringiensis and analysis of insecticidal activity].";
RL Sheng Wu Gong Cheng Xue Bao 18:687-692(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Chen J., Yu J., Pang Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY074706; AAL69542.1; -; Genomic DNA.
DR EMBL; AY187679; AAO32350.1; -; Genomic DNA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR003305; CBM_Cenc.
DR Pfam; PF02018; CBM_4_9; 1.
KM Oxidoreductase.
SQ SEQUENCE 789 AA; 88645 MW; D9DF334011551472 CRC64;

Query Match 5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 2.4e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 261 KTSGEVGNVNFLLIVLTALQAKAFLLTTCRKLGLADIDYT 303
Db 262 KTSGEVGNVNFLLIVLTALQAKAFLLTTCRKLGLADIDYT 304

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RESULT 10
Q58133_BACTU
ID Q58133_BACTU PRELIMINARY; PRT; 789 AA.
AC Q58133
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Vegetative insecticidal protein.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=9816C;
RA Cai J., Xiao L.;
RT "Bacillus thuringiensis strain 9816C vegetative insecticidal protein
gene."
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY945939; AAX9395.1; -; Genomic_DNA.
KW Oxidoreductase.
SQ SEQUENCE 789 AA; 88675 MW; 9F13448EAAE7C7AA CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 2; Length 789;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEGVNVPFLVLTALQAKAFLLTTCRKLGLADIDYT 303
DB 262 KTSGSEGVNVPFLVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 11
Q58X12_BACTU
ID Q58X12_BACTU PRELIMINARY; PRT; 789 AA.
AC Q58X12
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Vegetative insecticidal protein.
GN Name=vip3B;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Abdelkefi Mesrati L., Tounsi S., Jaoua S.;
RT "Characterization of a novel vip3-type gene from Bacillus
thuringiensis and evidence of its presence on a large plasmid."
RL FEMS Microbiol. Lett. 244:353-358(2005).
DR EMBL; AY739665; AAM65132.1; -; Genomic_DNA.
KW Oxidoreductase.
SQ SEQUENCE 789 AA; 88671 MW; ECB5355939FE76CA CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 2; Length 789;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEGVNVPFLVLTALQAKAFLLTTCRKLGLADIDYT 303
DB 262 KTSGSEGVNVPFLVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 12
Q938Z1_BACTU
ID Q938Z1_BACTU PRELIMINARY; PRT; 789 AA.
AC Q938Z1; O8L2N0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Vegetative insecticidal protein Vip3A (Vegetative insecticidal protein

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DE Vip3V).
GN Name=vip3A; Synonyms=vip3A-WB5, vip3V;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=6101, and 611;
RA Chen J., Yu J., Pang Y., Tang L.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Wu Y., Guan X.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB 50;
RX PubMed=15604775; DOI=10.1023/B:BITE.0000045645.4536.3f;
RA Wu Z.L., Guo W.Y., Qiu J.Z., Huang T.P., Li X.B., Guan X.;
RL "Cloning and localization of vip3A gene of Bacillus thuringiensis."
RT Biotechnol. Lett. 26:1425-1428(2004).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22244722; PubMed=12356474; DOI=10.1016/S1046-5928(02)00515-6;
RA Doss V.A., Anup Kumar K., Jayakumar R., Sekar V.;
RT "Cloning and expression of the vegetative insecticidal protein (vip3V)
gene of Bacillus thuringiensis in Escherichia coli."
RL Protein Expr. Purif. 26:82-88(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C9;
RA Liu R., Song F., Zhang J.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY074707; AAL69543.1; -; Genomic_DNA.
DR EMBL; AF500478; AAM22456.2; -; Genomic_DNA.
DR EMBL; AY295778; AAP51131.1; -; Genomic_DNA.
DR EMBL; AF373030; AAN60738.1; -; Genomic_DNA.
DR EMBL; AY489126; AAR35859.1; -; Genomic_DNA.
DR EMBL; AY074708; AAL69544.1; -; Genomic_DNA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR003305; Cenc_cabd_bd.
DR Pfam; PF02018; CBM_4_9; 1.
KW Oxidoreductase.
SQ SEQUENCE 789 AA; 88672 MW; 9DD746486623C7AE CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 2; Length 789;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEGVNVPFLVLTALQAKAFLLTTCRKLGLADIDYT 303
DB 262 KTSGSEGVNVPFLVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 13
Q4VYT0_BACTU
ID Q4VYT0_BACTU PRELIMINARY; PRT; 789 AA.
AC Q4VYT0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Vegetative insecticidal protein.
GN Name=vip3A;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BTAB51;
RA Pham N.B., Le N.H., Pham T.T., Chu H.H., Le B.T.;
RT "Cloning and sequence analysis gene encoding the vegetative

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RT Insecticidal protein (VIP3A) of some Vietnamese *B. thuringiensis* strains."  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ971413; CA196522.1; -; Genomic\_DNA.  
 DR InterPro: IPR003305; Cenc\_card\_bd.  
 DR Pfam: PF02018; CBM\_4\_9; 1.  
 KM Oxidoreductase.  
 SQ SEQUENCE 789 AA; 88614 MM; 5F255A098B9C86DD CRC64;

Query Match 5.5%; Score 43; DB 2; Length 789;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEGVNYYNPLIVLTALQAKAFLLTTCRKLGLADIDYT 303  
 |||||  
 DB 262 KTSGSEGVNYYNPLIVLTALQAKAFLLTTCRKLGLADIDYT 304

## RESULT 14

Q4U3F5\_BACTU  
 ID Q4U3F5\_BACTU PRELIMINARY; PRT; 789 AA.  
 AC Q4U3F5;  
 DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
 DE Vegetative insecticidal protein.  
 GN Name=VIP3A;  
 OS *Bacillus thuringiensis*.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC *Bacillus cereus* group.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=LS1;  
 RA Lu X., Hao H., Sun S., Zhu M., Du K., Li G.;  
 RT "Vegetative insecticidal protein gene vip3A-LS1 from *Bacillus thuringiensis* strain LS1."  
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: DQ016968; AA041427.1; -; Genomic\_DNA.  
 DR InterPro: IPR003305; Cenc\_card\_bd.  
 DR Pfam: PF02018; CBM\_4\_9; 1.  
 KM Oxidoreductase.  
 SQ SEQUENCE 789 AA; 88574 MM; A82803275AFEC19C CRC64;

Query Match 5.5%; Score 43; DB 2; Length 789;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEGVNYYNPLIVLTALQAKAFLLTTCRKLGLADIDYT 303  
 |||||  
 DB 262 KTSGSEGVNYYNPLIVLTALQAKAFLLTTCRKLGLADIDYT 304

## RESULT 15

Q4U3F4\_BACTU  
 ID Q4U3F4\_BACTU PRELIMINARY; PRT; 789 AA.  
 AC Q4U3F4;  
 DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
 DE Vegetative insecticidal protein.  
 GN Name=VIP3A;  
 OS *Bacillus thuringiensis*.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC *Bacillus cereus* group.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=LS8;  
 RA Lu X., Hao H., Sun S., Zhu M., Du K., Li G.;  
 RT "Vegetative insecticidal protein gene vip3A-LS8 from *Bacillus thuringiensis* strain LS8."  
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL: DQ016969; AA041428.1; -; Genomic\_DNA.  
 DR InterPro: IPR003305; Cenc\_card\_bd.  
 DR Pfam: PF02018; CBM\_4\_9; 1.  
 KM Oxidoreductase.  
 SQ SEQUENCE 789 AA; 88540 MM; D4A09EDA53898B3 CRC64;

Query Match 4.7%; Score 37; DB 2; Length 789;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-28;  
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 VGVNYYNPLIVLTALQAKAFLLTTCRKLGLADIDYT 303  
 |||||  
 DB 268 VGVNYYNPLIVLTALQAKAFLLTTCRKLGLADIDYT 304

Search completed: May 15, 2006, 20:55:35  
 Job time : 233 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 15, 2006, 20:55:51 ; Search time 47 Seconds  
(without alignments)  
1382.619 Million cell updates/sec

Title: US-10-698-096-17

Perfect score: 786  
Sequence: 1 MQNNKLTVKALPSFIDYFN.....VELSRASSRGVINGDFSIK 786

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size: 8

Total number of hits satisfying chosen parameters: 570988

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents AA: \*  
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2: /cgn2\_6/ptodata/1/iaa/6.COMB.pep: \*  
3: /cgn2\_6/ptodata/1/iaa/H.COMB.pep: \*  
4: /cgn2\_6/ptodata/1/iaa/PCITUS.COMB.pep: \*  
5: /cgn2\_6/ptodata/1/iaa/RR.COMB.pep: \*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	5.7	787	2	US-09-307-106-54 Sequence 54, Appl
2	43	5.5	511	2	US-09-002-285-88 Sequence 88, Appl
3	43	5.5	511	2	US-09-589-477-88 Sequence 88, Appl
4	43	5.5	511	2	US-10-099-285A-88 Sequence 88, Appl
5	43	5.5	759	2	US-09-002-285-86 Sequence 86, Appl
6	43	5.5	759	2	US-09-589-477-86 Sequence 86, Appl
7	43	5.5	759	2	US-10-099-285A-86 Sequence 86, Appl
8	43	5.5	789	2	US-08-960-780-6 Sequence 6, Appl
9	43	5.5	789	2	US-09-073-898-6 Sequence 6, Appl
10	43	5.5	789	2	US-09-002-285-80 Sequence 80, Appl
11	43	5.5	789	2	US-09-002-285-82 Sequence 82, Appl
12	43	5.5	789	2	US-09-002-285-84 Sequence 84, Appl
13	43	5.5	789	2	US-09-002-285-90 Sequence 90, Appl
14	43	5.5	789	2	US-09-002-285-92 Sequence 92, Appl
15	43	5.5	789	2	US-09-002-285-94 Sequence 94, Appl
16	43	5.5	789	2	US-09-002-285-96 Sequence 96, Appl
17	43	5.5	789	2	US-09-002-285-100 Sequence 100, Appl
18	43	5.5	789	2	US-09-589-477-80 Sequence 80, Appl
19	43	5.5	789	2	US-09-589-477-82 Sequence 82, Appl
20	43	5.5	789	2	US-09-589-477-84 Sequence 84, Appl
21	43	5.5	789	2	US-09-589-477-90 Sequence 90, Appl
22	43	5.5	789	2	US-09-589-477-92 Sequence 92, Appl
23	43	5.5	789	2	US-09-589-477-94 Sequence 94, Appl
24	43	5.5	789	2	US-09-589-477-96 Sequence 96, Appl
25	43	5.5	789	2	US-09-589-477-100 Sequence 100, Appl
26	43	5.5	789	2	US-09-850-351A-6 Sequence 6, Appl
27	43	5.5	789	2	US-10-099-285A-80 Sequence 80, Appl

28	43	5.5	789	2	US-10-099-285A-82 Sequence 82, Appl
29	43	5.5	789	2	US-10-099-285A-84 Sequence 84, Appl
30	43	5.5	789	2	US-10-099-285A-90 Sequence 90, Appl
31	43	5.5	789	2	US-10-099-285A-92 Sequence 92, Appl
32	43	5.5	789	2	US-10-099-285A-94 Sequence 94, Appl
33	43	5.5	789	2	US-10-099-285A-96 Sequence 96, Appl
34	43	5.5	789	2	US-10-099-285A-100 Sequence 100, Appl
35	43	5.5	790	2	US-08-960-780-4 Sequence 4, Appl
36	43	5.5	790	2	US-08-960-780-8 Sequence 8, Appl
37	43	5.5	790	2	US-09-073-898-4 Sequence 4, Appl
38	43	5.5	790	2	US-09-073-898-8 Sequence 8, Appl
39	43	5.5	790	2	US-09-002-285-102 Sequence 102, App
40	43	5.5	790	2	US-09-589-477-102 Sequence 2, Appl
41	43	5.5	790	2	US-09-307-106-2 Sequence 2, Appl
42	43	5.5	790	2	US-09-850-351A-4 Sequence 4, Appl
43	43	5.5	790	2	US-09-850-351A-8 Sequence 8, Appl
44	43	5.5	790	2	US-10-099-285A-102 Sequence 102, App
45	41	5.2	789	2	US-09-002-285-78 Sequence 78, Appl

#### ALIGNMENTS

RESULT 1  
US-09-307-106-54  
Sequence 54, Application US/09307106  
Patent No. 6603063  
GENERAL INFORMATION:  
APPLICANT: Feltelson, Jerald S.  
APPLICANT: Schnepf, H. Ernest  
APPLICANT: Narva, Kenneth B.  
APPLICANT: Stockhoff, Brian A.  
APPLICANT: Schmeltz, James  
APPLICANT: Loewer, David  
APPLICANT: Dullum, Charles Joseph  
APPLICANT: Muller-Cohn, Judy  
APPLICANT: Stamp, Lisa  
APPLICANT: Morrill, George  
TITLE OF INVENTION: No. 6603063el Pesticidal Toxins and Nucleotide  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/307,106  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/960,780  
FILING DATE: 30-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/073,898  
FILING DATE: 05-MAY-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-708C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100

TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 787 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-307-106-54

Query Match 5.7%; Score 45; DB 2; Length 787;  
Best Local Similarity 100.0%; Pred. No. 4.3e-37;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 EYLSKQLKEISDKLDVINNVVLINSTITTETTPAYORIKYNEKFE 183  
Db 140 EYLSKQLKEISDKLDVINNVVLINSTITTETTPAYORIKYNEKFE 184

RESULT 2  
US-09-002-285-88

Sequence 88, Application US/09002285  
Patent No. 6369213

GENERAL INFORMATION:

APPLICANT: Schnepf, H. Ernest

APPLICANT: Wicker, Carol

APPLICANT: Narva, Kenneth E.

APPLICANT: Walz, Michelle

APPLICANT: Stockhoff, Brian

APPLICANT: Muller-Cohn, Judy

TITLE OF INVENTION: Toxins Active Against Pests

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:  
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/002,285

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/886,615

FILING DATE: 1-JUL-1997

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/674,002

FILING DATE: 1-JUL-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-701C2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100

TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 88:

SEQUENCE CHARACTERISTICS:  
LENGTH: 511 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein  
US-09-002-285-88

Query Match 5.5%; Score 43; DB 2; Length 511;  
Best Local Similarity 100.0%; Pred. No. 3.3e-35;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVYVFLIVLTALQAKFLTTTCRKLGLADIDYT 303  
Db 122 KTSGEVGNVYVFLIVLTALQAKFLTTTCRKLGLADIDYT 164

RESULT 3  
US-09-589-477-88  
Sequence 88, Application US/09589477  
Patent No. 6570005

GENERAL INFORMATION:

APPLICANT: Schnepf, H. Ernest

APPLICANT: Wicker, Carol

APPLICANT: Narva, Kenneth E.

APPLICANT: Walz, Michelle

APPLICANT: Stockhoff, Brian

TITLE OF INVENTION: Toxins Active Against Pests

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:  
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/589,477

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/886,615

FILING DATE: 1-JUL-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/674,002

FILING DATE: 1-JUL-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-701C1C1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100

TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 88:

SEQUENCE CHARACTERISTICS:  
LENGTH: 511 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein  
US-09-589-477-88

Query Match 5.5%; Score 43; DB 2; Length 511;  
Best Local Similarity 100.0%; Pred. No. 3.3e-35;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGEVGNVYVFLIVLTALQAKFLTTTCRKLGLADIDYT 303  
Db 122 KTSGEVGNVYVFLIVLTALQAKFLTTTCRKLGLADIDYT 164

RESULT 4  
US-10-099-285A-88

Sequence 88, Application US/10099285A  
Patent No. 6752992

GENERAL INFORMATION:

APPLICANT: Schnepf, H. Ernest

```

Wicker, Carol
Narva, Kenneth E.
Walz, Michelle
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285A
FILING DATE: 02-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/002,285
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-10-099-285A-88
Query Match 5.5%; Score 43; DB 2; Length 511;
Best Local Similarity 100.0%; Pred. No. 3.3e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 261 KTGSGSEGVNPNFLIVLTALQAKAFLLTTCRLLGLADIDYT 303
DB 122 KTGSGSEGVNPNFLIVLTALQAKAFLLTTCRLLGLADIDYT 164
RESULT 5
US-09-002-285-86
Sequence 86, Application US/09002285
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
```

```

STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 372-5800
TELEFAX: (352) 375-8100
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 759 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-002-285-86
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```

Query Match 5.5%; Score 43; DB 2; Length 759;
Best Local Similarity 100.0%; Pred. No. 4.8e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 261 KTGSGSEGVNPNFLIVLTALQAKAFLLTTCRLLGLADIDYT 303
DB 262 KTGSGSEGVNPNFLIVLTALQAKAFLLTTCRLLGLADIDYT 304
```

```

US-09-589-477-86
Sequence 86, Application US/09589477
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,477
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
```

FILING DATE: 1-JUL-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/674,002  
FILING DATE: 1-JUL-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-701C1C1  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 759 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-589-477-86

Query Match 5.5%; Score 43; DB 2; Length 759;  
Best Local Similarity 100.0%; Pred. No. 4.8e-35;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEVGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 303  
DB 262 KTSGSEVGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 7  
US-10-099-285A-86  
Sequence 86, Application US/10099285A  
Patent No. 6752992  
GENERAL INFORMATION:  
APPLICANT: Schneck, H. Ernest  
Wicker, Carol  
Narva, Kenneth E.  
Waltz, Michelle  
Stockhoff, Brian  
Muller-Cohn, Judy  
TITLE OF INVENTION: Toxins Active Against Pests  
NUMBER OF SEQUENCES: 105  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/099,285A  
FILING DATE: 02-Jul-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/002,285  
FILING DATE: 31-DEC-1997  
APPLICATION NUMBER: US 08/886,615  
FILING DATE: 1-JUL-1997  
APPLICATION NUMBER: US 08/674,002  
FILING DATE: 1-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-701C2D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100

TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 759 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 86:  
US-10-099-285A-86

Query Match 5.5%; Score 43; DB 2; Length 759;  
Best Local Similarity 100.0%; Pred. No. 4.8e-35;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEVGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 303  
DB 262 KTSGSEVGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 304

RESULT 8  
US-08-960-780-6  
Sequence 6, Application US/08960780  
Patent No. 6204435  
GENERAL INFORMATION:  
APPLICANT: Feltelson, Jerald S.  
APPLICANT: Schneck, H. Ernest  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Stockhoff, Brian A.  
APPLICANT: Schmeltz, James  
APPLICANT: Loewer, David  
APPLICANT: Dullum, Charles Joseph  
APPLICANT: Muller-Cohn, Judy  
APPLICANT: Stamp, Lisa  
TITLE OF INVENTION: No. 6204435e1 Pesticidal Toxins and Nucleotide  
NUMBER OF SEQUENCES: 134  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/960,780  
FILING DATE: 30-OCT-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: MA-708  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 81Pd  
US-08-960-780-6

Query Match 5.5%; Score 43; DB 2; Length 789;  
Best Local Similarity 100.0%; Pred. No. 4.9e-35;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTGSEGVNYYNFIIVLTALQAKAFLLTTCRKLGLADIYDT 303  
DB 262 KTGSEGVNYYNFIIVLTALQAKAFLLTTCRKLGLADIYDT 304

## RESULT 9

US-09-073-898-6  
; Sequence 6, Application US/09073898  
; Patent No. 6242669  
; GENERAL INFORMATION:  
; APPLICANT: Petelerson, Jerald S.  
; APPLICANT: Schnepf, H. Ernest  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Stockhoff, Brian A.  
; APPLICANT: Schmeits, James  
; APPLICANT: Loewer, David  
; APPLICANT: Dullum, Charles Joseph  
; APPLICANT: Muller-Cohn, Judy  
; APPLICANT: Stamp, Lisa  
; APPLICANT: Morrill, George  
; APPLICANT: Finstad-Lee, Stacey  
; TITLE OF INVENTION: No. 624269el Pesticidal Toxins and Nucleotide  
; NUMBER OF SEQUENCES: 144  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: US  
; ZIP: 32606-6669  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/073,898  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/029,848  
; FILING DATE: 30-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/960,780  
; FILING DATE: 30-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sanders, Jay M.  
; REGISTRATION NUMBER: 39,355  
; REFERENCE/DOCKET NUMBER: MA-708C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 352-375-8100  
; TELEFAX: 352-372-5800  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 789 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: 81F4  
; US-09-073-898-6

Query Match 5.5%; Score 43; DB 2; Length 789;  
Best Local Similarity 100.0%; Pred. No. 4.9e-35;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTGSEGVNYYNFIIVLTALQAKAFLLTTCRKLGLADIYDT 303  
DB 262 KTGSEGVNYYNFIIVLTALQAKAFLLTTCRKLGLADIYDT 304

## RESULT 10

US-09-002-285-80  
; Sequence 80, Application US/09002285  
; Patent No. 6369213  
; GENERAL INFORMATION:  
; APPLICANT: Schnepf, H. Ernest  
; APPLICANT: Wicker, Carol  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Walz, Michelle  
; APPLICANT: Stockhoff, Brian  
; APPLICANT: Muller-Cohn, Judy  
; TITLE OF INVENTION: Toxins Active Against Peets  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/002,285  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/886,615  
; FILING DATE: 1-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/674,002  
; FILING DATE: 1-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sanders, Jay M.  
; REGISTRATION NUMBER: 39,355  
; REFERENCE/DOCKET NUMBER: MA-701C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 80:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 789 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-002-285-80

Query Match 5.5%; Score 43; DB 2; Length 789;  
Best Local Similarity 100.0%; Pred. No. 4.9e-35;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTGSEGVNYYNFIIVLTALQAKAFLLTTCRKLGLADIYDT 303  
DB 262 KTGSEGVNYYNFIIVLTALQAKAFLLTTCRKLGLADIYDT 304

## RESULT 11

US-09-002-285-82  
; Sequence 82, Application US/09002285  
; Patent No. 6369213  
; GENERAL INFORMATION:  
; APPLICANT: Schnepf, H. Ernest  
; APPLICANT: Wicker, Carol  
; APPLICANT: Narva, Kenneth E.

```

/ APPLICANT: Walz, Michelle
/ APPLICANT: Stockhoff, Brian
/ APPLICANT: Muller-Cohn, Judy
/ TITLE OF INVENTION: Toxins Active Against Pests
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/002,285
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/886,615
/ FILING DATE: 1-JUL-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/674,002
/ FILING DATE: 1-JUL-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sanders, Jay M.
/ REGISTRATION NUMBER: 39,355
/ REFERENCE/DOCKET NUMBER: MA-701C2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (352) 375-8100
/ TELEFAX: (352) 372-5800
/ INFORMATION FOR SEQ ID NO: 82:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 789 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-002-285-82

Query Match          5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 4.9e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      261 KTGSGEVGVNPLIVLTALQAKAFILTTTCRKLGLADIDYT 303
DB      262 KTGSGEVGVNPLIVLTALQAKAFILTTTCRKLGLADIDYT 304

RESULT 12
US-09-002-285-84
/ Sequence 84, Application US/09002285
/ Patent No. 6369213
/ GENERAL INFORMATION:
/ APPLICANT: Schnepf, H. Ernest
/ APPLICANT: Wicker, Carol
/ APPLICANT: Narva, Kenneth E.
/ APPLICANT: Walz, Michelle
/ APPLICANT: Stockhoff, Brian
/ APPLICANT: Muller-Cohn, Judy
/ TITLE OF INVENTION: Toxins Active Against Pests
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/002,285
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/886,615
/ FILING DATE: 1-JUL-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/674,002
/ FILING DATE: 1-JUL-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sanders, Jay M.
/ REGISTRATION NUMBER: 39,355
/ REFERENCE/DOCKET NUMBER: MA-701C2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (352) 375-8100
/ TELEFAX: (352) 372-5800
/ INFORMATION FOR SEQ ID NO: 84:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 789 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-002-285-84

Query Match          5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 4.9e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      261 KTGSGEVGVNPLIVLTALQAKAFILTTTCRKLGLADIDYT 303
DB      262 KTGSGEVGVNPLIVLTALQAKAFILTTTCRKLGLADIDYT 304

RESULT 13
US-09-002-285-90
/ Sequence 90, Application US/09002285
/ Patent No. 6369213
/ GENERAL INFORMATION:
/ APPLICANT: Schnepf, H. Ernest
/ APPLICANT: Wicker, Carol
/ APPLICANT: Narva, Kenneth E.
/ APPLICANT: Walz, Michelle
/ APPLICANT: Stockhoff, Brian
/ APPLICANT: Muller-Cohn, Judy
/ TITLE OF INVENTION: Toxins Active Against Pests
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/002,285
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/886,615
/ FILING DATE: 1-JUL-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/674,002
/ FILING DATE: 1-JUL-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sanders, Jay M.
/ REGISTRATION NUMBER: 39,355
/ REFERENCE/DOCKET NUMBER: MA-701C2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (352) 375-8100
/ TELEFAX: (352) 372-5800
/ INFORMATION FOR SEQ ID NO: 84:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 789 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-002-285-84
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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/002,285
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/886,615
/ FILING DATE: 1-JUL-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/674,002
/ FILING DATE: 1-JUL-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sanders, Jay M.
/ REGISTRATION NUMBER: 39,355
/ REFERENCE/DOCKET NUMBER: MA-701C2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (352) 375-8100
/ TELEFAX: (352) 372-5800
/ INFORMATION FOR SEQ ID NO: 84:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 789 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-002-285-84

Query Match          5.5%; Score 43; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 4.9e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      261 KTGSGEVGVNPLIVLTALQAKAFILTTTCRKLGLADIDYT 303
DB      262 KTGSGEVGVNPLIVLTALQAKAFILTTTCRKLGLADIDYT 304

RESULT 13
US-09-002-285-90
/ Sequence 90, Application US/09002285
/ Patent No. 6369213
/ GENERAL INFORMATION:
/ APPLICANT: Schnepf, H. Ernest
/ APPLICANT: Wicker, Carol
/ APPLICANT: Narva, Kenneth E.
/ APPLICANT: Walz, Michelle
/ APPLICANT: Stockhoff, Brian
/ APPLICANT: Muller-Cohn, Judy
/ TITLE OF INVENTION: Toxins Active Against Pests
/ NUMBER OF SEQUENCES: 105
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/002,285
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/886,615
/ FILING DATE: 1-JUL-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/674,002
/ FILING DATE: 1-JUL-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sanders, Jay M.
/ REGISTRATION NUMBER: 39,355
/ REFERENCE/DOCKET NUMBER: MA-701C2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (352) 375-8100
/ TELEFAX: (352) 372-5800
/ INFORMATION FOR SEQ ID NO: 84:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 789 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-002-285-84
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;; FILING DATE: 1-JUL-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sanders, Jay M.  
;; REGISTRATION NUMBER: 39,355  
;; REFERENCE/DOCKET NUMBER: MA-701C2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (352) 375-8100  
;; TELEFAX: (352) 372-5800  
;; INFORMATION FOR SEQ ID NO: 90:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 789 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-09-002-285-90

Query Match  
Best Local Similarity 100.0%; Pred. No. 4.9e-35;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKILGLADIDYT 303  
DB 262 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKILGLADIDYT 304

RESULT 14  
US-09-002-285-92  
; Sequence 92, Application US/09002285  
; Patent No. 6369213  
; GENERAL INFORMATION:  
; APPLICANT: Schnepf, H. Ernest  
; APPLICANT: Wicker, Carol  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Walz, Michelle  
; APPLICANT: Stockhoff, Brian  
; APPLICANT: Muller-Cohn, Judy  
; TITLE OF INVENTION: Toxins Active Against Pests  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentlin  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/002,285  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/886,615  
; FILING DATE: 1-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/674,002  
; FILING DATE: 1-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sanders, Jay M.  
; REGISTRATION NUMBER: 39,355  
; REFERENCE/DOCKET NUMBER: MA-701C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 92:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 789 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-09-002-285-92

Query Match  
Best Local Similarity 100.0%; Pred. No. 4.9e-35;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKILGLADIDYT 303  
DB 262 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKILGLADIDYT 304

RESULT 15  
US-09-002-285-94  
; Sequence 94, Application US/09002285  
; Patent No. 6369213  
; GENERAL INFORMATION:  
; APPLICANT: Schnepf, H. Ernest  
; APPLICANT: Wicker, Carol  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Walz, Michelle  
; APPLICANT: Stockhoff, Brian  
; APPLICANT: Muller-Cohn, Judy  
; TITLE OF INVENTION: Toxins Active Against Pests  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentlin  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/002,285  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/886,615  
; FILING DATE: 1-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/674,002  
; FILING DATE: 1-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sanders, Jay M.  
; REGISTRATION NUMBER: 39,355  
; REFERENCE/DOCKET NUMBER: MA-701C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 94:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 789 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-002-285-94

Query Match  
Best Local Similarity 100.0%; Pred. No. 4.9e-35;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKILGLADIDYT 303  
DB 262 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKILGLADIDYT 304

Tue May 16 14:47:42 2006

us-10-698-096-17.oli.rat

Page 8

Search completed: May 15, 2006, 20:57:18  
Job time : 48 secs

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OM protein - protein search, using sw model

Run on: May 15, 2006, 20:56:41 ; Search time 169 Seconds  
(without alignments)  
1943.277 Million cell updates/sec

Title: US-10-698-096-17  
Perfect score: 786  
Sequence: 1 MOKNNKLSVYALPSFIDYFN.....VELSRASSRGVINGDFSIK 786

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1866650

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	786	100.0	786	4 US-10-698-096-17	Sequence 17, App1
2	45	5.7	787	4 US-10-452-002A-54	Sequence 54, App1
3	45	5.7	787	4 US-10-698-096-25	Sequence 25, App1
4	45	5.7	788	4 US-10-698-096-27	Sequence 27, App1
5	43	5.5	511	4 US-10-099-285-86	Sequence 86, App1
6	43	5.5	759	4 US-10-099-285-86	Sequence 86, App1
7	43	5.5	786	4 US-10-698-096-19	Sequence 19, App1
8	43	5.5	787	4 US-10-473-687-2	Sequence 2, App1
9	43	5.5	787	4 US-10-473-687-7	Sequence 7, App1
10	43	5.5	787	4 US-10-505-315-7	Sequence 11, App1
11	43	5.5	788	5 US-10-505-315-11	Sequence 11, App1
12	43	5.5	788	5 US-10-505-315-32	Sequence 32, App1
13	43	5.5	789	3 US-09-850-351A-6	Sequence 6, App1
14	43	5.5	789	4 US-10-099-285-80	Sequence 80, App1
15	43	5.5	789	4 US-10-099-285-82	Sequence 82, App1
16	43	5.5	789	4 US-10-099-285-84	Sequence 84, App1
17	43	5.5	789	4 US-10-099-285-90	Sequence 90, App1
18	43	5.5	789	4 US-10-099-285-92	Sequence 92, App1
19	43	5.5	789	4 US-10-099-285-94	Sequence 94, App1
20	43	5.5	789	4 US-10-099-285-96	Sequence 96, App1
21	43	5.5	789	4 US-10-099-285-100	Sequence 100, App1
22	43	5.5	789	4 US-10-698-096-6	Sequence 6, App1
23	43	5.5	789	4 US-10-473-687-5	Sequence 5, App1
24	43	5.5	789	5 US-10-505-315-5	Sequence 5, App1
25	43	5.5	790	3 US-09-850-351A-4	Sequence 4, App1
26	43	5.5	790	3 US-09-850-351A-8	Sequence 8, App1
27	43	5.5	790	4 US-10-099-285-102	Sequence 102, App1

28	43	5.5	790	4 US-10-452-002A-2	Sequence 2, App1
29	43	5.5	790	4 US-10-698-096-4	Sequence 4, App1
30	43	5.5	790	4 US-10-698-096-8	Sequence 8, App1
31	41	5.2	789	4 US-10-099-285-78	Sequence 78, App1
32	38	4.8	788	5 US-10-505-315-2	Sequence 2, App1
33	35	4.5	789	3 US-09-904-226-2	Sequence 2, App1
34	35	4.5	789	3 US-10-099-285-98	Sequence 98, App1
35	32	4.1	789	3 US-09-904-226-4	Sequence 4, App1
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37	29	3.7	801	5 US-10-505-315-9	Sequence 9, App1
38	9	1.1	1381	4 US-10-369-493-1417	Sequence 1417, App1
39	9	1.1	3753	3 US-09-980-217-29	Sequence 29, App1
40	8	1.0	72	4 US-10-425-115-312302	Sequence 312302, App1
41	8	1.0	111	3 US-09-738-626-4031	Sequence 4031, App1
42	8	1.0	359	3 US-09-712-363-269	Sequence 269, App1
43	8	1.0	461	4 US-10-282-122A-54522	Sequence 54522, App1
44	8	1.0	485	4 US-10-156-761-11034	Sequence 11034, App1
45	8	1.0	582	4 US-10-369-493-13500	Sequence 13500, App1

## ALIGNMENTS

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RESULT 1
US-10-698-096-17
; Sequence 17, Application US/10698096
; Publication No. US20040128716A1
; GENERAL INFORMATION:
; APPLICANT: Merlo, Donald
; TITLE OF INVENTION: Polynucleotides, Pesticidal Proteins, and Novel Methods of Using
; FILE REFERENCE: NA-708C01
; CURRENT APPLICATION NUMBER: US/10/698,096
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 09/850,351
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 09/073,898
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 08/690,780
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,848
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-698-096-17

Query Match      100.0%; Score 786; DB 4; Length 786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOKNNKLSVYALPSFIDYFNIGYGFATGKIDINNMIFKNTGGDLTLDLTKQOLNFI 60
DB 1 MOKNNKLSVYALPSFIDYFNIGYGFATGKIDINNMIFKNTGGDLTLDLTKQOLNFI 60
QY 61 SGKLDVNGSINDLAQGNLDTELSEIKELIKIANQKRVINDVTKDAINMLMTYLPKI 120
DB 61 SGKLDVNGSINDLAQGNLDTELSEIKELIKIANQKRVINDVTKDAINMLMTYLPKI 120
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DB 121 TSMLSVPMQNVYALGQIEYLSKQKEISDKLDVINNVYLNSTLTETPAYQRIKYNE 180
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DB 181 KPEALTSATETNKTQDSSHDIDDELTELTELASVTKNDVGEFYANTFHDWIGN 240
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DB 241 NLFGRSALKTASLILAKENIKTSGSEVGVNVPFLIVLTALQAKAFITLTTCRKLGLADI 300

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DB 301 DYPINMEHLNKEKEEERVNILPTLSNTFSNPYKARSGDKDAKIMEAKPGYALVGF 360
QY 361 ISKDSIAVLKVYQAKLKANYQIDKDSISEIYVGDIDKLLCPDSEQWYTNKIAFPNEYV 420
DB 361 ISKDSIAVLKVYQAKLKANYQIDKDSISEIYVGDIDKLLCPDSEQWYTNKIAFPNEYV 420
QY 421 ITTIAFTKULNSLRVEYTAFFYDSSTGDIANKKTISSSEAFESMLNANDGYVMPIGTI 480
DB 421 ITTIAFTKULNSLRVEYTAFFYDSSTGDIANKKTISSSEAFESMLNANDGYVMPIGTI 480
QY 481 SETFLPPIINGFGLVVDENSRVLVTLCSTYLRETLATLDSNKKTKLIVPNGFISINVEN 540
DB 481 SETFLPPIINGFGLVVDENSRVLVTLCSTYLRETLATLDSNKKTKLIVPNGFISINVEN 540
QY 541 GNLGEGNLEPWKANNKRAYVDHTGTVNGTYKVLVYHEDGFSQITGDKLKLTETVITQYIV 600
DB 541 GNLGEGNLEPWKANNKRAYVDHTGTVNGTYKVLVYHEDGFSQITGDKLKLTETVITQYIV 600
QY 601 KGRKAIYLDKDKNGDYIYEEETNNLEDEQAVTKRFTITGDSRVHLIFTSONGEAPFGN 660
DB 601 KGRKAIYLDKDKNGDYIYEEETNNLEDEQAVTKRFTITGDSRVHLIFTSONGEAPFGN 660
QY 661 FIISEIRPSEBLLSPELIKSDAWVSGQTIWISGNSINSNVNGTFRQNLISLSYSTYSM 720
DB 661 FIISEIRPSEBLLSPELIKSDAWVSGQTIWISGNSINSNVNGTFRQNLISLSYSTYSM 720
QY 721 NFNVNGFGKTYTINSREVVFERSYLOPSSKYISEKTTTNTTGLVYELSRASSRGVINE 780
DB 721 NFNVNGFGKTYTINSREVVFERSYLOPSSKYISEKTTTNTTGLVYELSRASSRGVINE 780
QY 781 GDFSIR 786
DB 781 GDFSIR 786
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RESULT 2
US-10-452-002A-54
; Sequence 54, Application US/10452002A
; Publication No. US20030236195A1
; GENERAL INFORMATION:
; APPLICANT: Gerald S. Feltelson
; APPLICANT: H. Ernest Schmelef
; APPLICANT: Kenneth E. Narva
; APPLICANT: Brian A. Stockhoff
; APPLICANT: James L. Schmeltz
; APPLICANT: David Loewer
; APPLICANT: Charles J. Dullum
; APPLICANT: Judy Muller-Cohn
; APPLICANT: Lisa Stamp
; APPLICANT: George Morrill
; APPLICANT: Stacey Finstad Lee
; TITLE OF INVENTION: No. US20030236195A1e1 Pesticidal Proteins and Methods of Using Th
; FILE REFERENCE: MA708CD21
; CURRENT APPLICATION NUMBER: US/10/452,002A
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/307,106
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 09/073,898
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 08/960,780
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: 60/029,848
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 54
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis strain KB59A4-6
US-10-452-002A-54
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Query Match 5.7%; Score 45; DB 4; Length 787;
Best Local Similarity 100.0%; Pred. No. 7e-34; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 139 EYLSKQKEISDKLDVINVNVILNSTLTETTPAYQRIKYVNEKFE 183
DB 140 EYLSKQKEISDKLDVINVNVILNSTLTETTPAYQRIKYVNEKFE 184

RESULT 3
US-10-698-096-25
; Sequence 25, Application US/10698096
; Publication No. US20040128716A1
; GENERAL INFORMATION:
; APPLICANT: Narva, Kenneth
; APPLICANT: Merlo, Donald
; TITLE OF INVENTION: Polynucleotides, Pesticidal Proteins, and Novel Methods of Using
; FILE REFERENCE: MA-708CDCl
; CURRENT APPLICATION NUMBER: US/10/698,096
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 09/850,351
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 09/073,898
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 08/690,780
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,848
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 25
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-698-096-25
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Query Match 5.7%; Score 45; DB 4; Length 787;
Best Local Similarity 100.0%; Pred. No. 7e-34; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 139 EYLSKQKEISDKLDVINVNVILNSTLTETTPAYQRIKYVNEKFE 183
DB 140 EYLSKQKEISDKLDVINVNVILNSTLTETTPAYQRIKYVNEKFE 184

RESULT 4
US-10-698-096-27
; Sequence 27, Application US/10698096
; Publication No. US20040128716A1
; GENERAL INFORMATION:
; APPLICANT: Narva, Kenneth
; APPLICANT: Merlo, Donald
; TITLE OF INVENTION: Polynucleotides, Pesticidal Proteins, and Novel Methods of Using
; FILE REFERENCE: MA-708CDCl
; CURRENT APPLICATION NUMBER: US/10/698,096
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 09/850,351
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 09/073,898
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 08/690,780
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/029,848
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 27
; LENGTH: 788
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-698-096-27
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Query Match 5.7%; Score 45; DB 4; Length 788;  
Best Local Similarity 100.0%; Pred. No. 7e-34;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 EYLSKQLEISDKLDVINNVNLTITETIPAYORIRYVNEKFE 183  
DB 141 EYLSKQLEISDKLDVINNVNLTITETIPAYORIRYVNEKFE 185

## RESULT 5

US-10-099-285-88

Sequence 88, Application US/10099285  
Publication No. US20030105319A1  
GENERAL INFORMATION:

APPLICANT: Schnepf, H. Ernest

Wicker, Carol

Narva, Kenneth E.

Walz, Michelle

Stochoff, Brian

Muller-Cohn, Judy

TITLE OF INVENTION: Toxins Active Against Pests

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESSES:

ADDRESS: Saliwanchik, Lloyd &amp; Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/099,285

FILING DATE: 15-Mar-2002

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/002,285

FILING DATE: &lt;Unknown&gt;

APPLICATION NUMBER: US 08/886,615

FILING DATE: 1-JUL-1997

APPLICATION NUMBER: US 08/674,002

FILING DATE: 1-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-701C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (352) 375-8100

TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 88:

SEQUENCE CHARACTERISTICS:

LENGTH: 511 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 88:

US-10-099-285-88

Query Match 5.5%; Score 43; DB 4; Length 511;

Best Local Similarity 100.0%; Pred. No. 4e-32;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSSEVGNVYNPLIVLTALQAKAFLLTTCRKLGLADIDYT 303

DB 122 KTSSEVGNVYNPLIVLTALQAKAFLLTTCRKLGLADIDYT 164

## RESULT 6

US-10-099-285-86

Sequence 86, Application US/10099285  
Publication No. US20030105319A1  
GENERAL INFORMATION:

APPLICANT: Schnepf, H. Ernest

Wicker, Carol

Narva, Kenneth E.

Walz, Michelle

Stochoff, Brian

Muller-Cohn, Judy

TITLE OF INVENTION: Toxins Active Against Pests

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESSES:

ADDRESS: Saliwanchik, Lloyd &amp; Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/099,285

FILING DATE: 15-Mar-2002

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/002,285

FILING DATE: &lt;Unknown&gt;

APPLICATION NUMBER: US 08/886,615

FILING DATE: 1-JUL-1997

APPLICATION NUMBER: US 08/674,002

FILING DATE: 1-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-701C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (352) 375-8100

TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 86:

SEQUENCE CHARACTERISTICS:

LENGTH: 759 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 86:

US-10-099-285-86

Query Match 5.5%; Score 43; DB 4; Length 759;

Best Local Similarity 100.0%; Pred. No. 5.7e-32;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSSEVGNVYNPLIVLTALQAKAFLLTTCRKLGLADIDYT 303

DB 262 KTSSEVGNVYNPLIVLTALQAKAFLLTTCRKLGLADIDYT 304

## RESULT 7

US-10-698-096-19

Sequence 19, Application US/10698096  
Publication No. US20040128716A1  
GENERAL INFORMATION:

APPLICANT: Narva, Kenneth

TITLE OF INVENTION: Polynucleotides, Pesticidal Proteins, and Novel Methods of Using

FILE REFERENCE: MA-708C01

CURRENT APPLICATION NUMBER: US/10/698,096

CURRENT FILING DATE: 2003-10-31

PRIOR APPLICATION NUMBER: US 09/850,351

PRIOR FILING DATE: 2001-05-07



TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Hybrid Vip3a-C toxin  
US-10-505-315-11

Query Match 5.5%; Score 43; DB 5; Length 788;  
Best Local Similarity 100.0%; Pred. No. 5.9e-32;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEGVNYPFLIVLTALQAKAFLLTTCRKLGADIDYT 303  
DB 262 KTSGSEGVNYPFLIVLTALQAKAFLLTTCRKLGADIDYT 304

RESULT 12  
US-10-505-315-32  
Sequence 32, Application US/10505315  
Publication No. US20050210545A1  
GENERAL INFORMATION:  
APPLICANT: Syngenta Participations AG  
APPLICANT: Shen, Zhicheng  
APPLICANT: Warren, Gregory  
APPLICANT: Shockoski, Frank  
APPLICANT: Kramer, Vance  
TITLE OF INVENTION: Novel Vip3 Toxins and Methods of Use  
FILE REFERENCE: 60163PCT  
CURRENT APPLICATION NUMBER: US/10/505,315  
PRIORITY FILING DATE: 2004-08-19  
PRIORITY APPLICATION NUMBER: US 60/362250  
PRIORITY FILING DATE: 2002-03-06  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 32  
LENGTH: 788  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (1)-(788)  
OTHER INFORMATION: Vip3c-12168 toxin  
US-10-505-315-32

Query Match 5.5%; Score 43; DB 5; Length 788;  
Best Local Similarity 100.0%; Pred. No. 5.9e-32;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEGVNYPFLIVLTALQAKAFLLTTCRKLGADIDYT 303  
DB 262 KTSGSEGVNYPFLIVLTALQAKAFLLTTCRKLGADIDYT 304

RESULT 13  
US-09-850-351A-6  
Sequence 6, Application US/09850351A  
Patent No. US2002010080A1  
GENERAL INFORMATION:  
APPLICANT: Feteleson, Jerald S.  
Schnepf, H. Ernest  
Narva, Kenneth E.  
Stockhoff, Brian A.  
Schmeits, James  
Loewer, David  
Dullum, Charles Joseph  
Muller-Cohn, Judy  
Stamp, Lisa  
Morrill, George  
TITLE OF INVENTION: No. US2002010080A1 Pesticidal Toxins and Nucleotide  
Sequences Which Encode These Toxins  
NUMBER OF SEQUENCES: 144  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606-6669  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/850,351A  
FILING DATE: 07-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/073,898  
FILING DATE: 06-MAY-1998  
APPLICATION NUMBER: US 08/960,780  
FILING DATE: 30-OCT-1997  
APPLICATION NUMBER: US 60/029,848  
FILING DATE: 30-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: WA-708CD1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 81F  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-850-351A-6  
Query Match 5.5%; Score 43; DB 3; Length 789;  
Best Local Similarity 100.0%; Pred. No. 5.9e-32;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 KTSGSEGVNYPFLIVLTALQAKAFLLTTCRKLGADIDYT 303  
DB 262 KTSGSEGVNYPFLIVLTALQAKAFLLTTCRKLGADIDYT 304

RESULT 14  
US-10-099-285-80  
Sequence 80, Application US/10099285  
Publication No. US20030105319A1  
GENERAL INFORMATION:  
APPLICANT: Schnepf, H. Ernest  
Wicker, Carol  
Narva, Kenneth E.  
Walz, Michelle  
Stockhoff, Brian  
Muller-Cohn, Judy  
TITLE OF INVENTION: Toxins Active Against Pests  
NUMBER OF SEQUENCES: 105  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
STATE: Florida  
CITY: Gainesville  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn

;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/099,285  
;; FILING DATE: 15-Mar-2002  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/002,285  
;; FILING DATE: <Unknown>  
;; APPLICATION NUMBER: US 08/886,615  
;; FILING DATE: 1-JUL-1997  
;; APPLICATION NUMBER: US 08/674,002  
;; FILING DATE: 1-JUL-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sanders, Jay M.  
;; REGISTRATION NUMBER: 39,355  
;; REFERENCE/DOCKET NUMBER: MA-701C2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (352) 375-8100  
;; TELEFAX: (352) 372-5800  
;; INFORMATION FOR SEQ ID NO: 80:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 789 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 80:  
US-10-099-285-80  
  
Query Match 5.5%; Score 43; DB 4; Length 789;  
Best Local Similarity 100.0%; Pred. No. 5.9e-32;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 261 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 303  
DB 262 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 304  
  
RESULT 15  
US-10-099-285-82  
; Sequence 82, Application US/10099285  
; Publication No. US20030105319A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmeff, H. Ernest  
; Wicker, Carol  
; Narva, Kenneth E.  
; Walz, Michelle  
; Stockhoff, Brian  
; Muller-Cohn, Judy  
; TITLE OF INVENTION: Toxins Active Against Pests  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentlin  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/099,285  
; FILING DATE: 15-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/002,285  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/886,615  
; FILING DATE: 1-JUL-1997  
; APPLICATION NUMBER: US 08/674,002  
; FILING DATE: 1-JUL-1996

;;  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sanders, Jay M.  
;; REGISTRATION NUMBER: 39,355  
;; REFERENCE/DOCKET NUMBER: MA-701C2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (352) 375-8100  
;; TELEFAX: (352) 372-5800  
;; INFORMATION FOR SEQ ID NO: 82:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 789 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 82:  
US-10-099-285-82  
  
Query Match 5.5%; Score 43; DB 4; Length 789;  
Best Local Similarity 100.0%; Pred. No. 5.9e-32;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 261 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 303  
DB 262 KTSGSEGVNPNFLIVLTALQAKAFLLTTCRKLGLADIDYT 304

Search completed: May 15, 2006, 21:00:13  
Job time : 171 secs

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 15, 2006, 20:57:31 ; Search time 30 Seconds  
(without alignments)  
1230.060 Million cell updates/sec

Title: US-10-698-096-17

Perfect score: 786  
Sequence: 1 MOKNNKLXVALPSFIDYFN.....VELSRASSGVINFGDFSIK 786

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250120

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications\_AA\_New:\*  
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2: /SIDS5/ptodata/1/pubpaa/US06\_NEW\_PUB.pep1:\*  
3: /SIDS5/ptodata/1/pubpaa/US07\_NEW\_PUB.pep1:\*  
4: /SIDS5/ptodata/1/pubpaa/US08\_NEW\_PUB.pep1:\*  
5: /SIDS5/ptodata/1/pubpaa/ECT\_NEW\_PUB.pep1:\*  
6: /SIDS5/ptodata/1/pubpaa/US09\_NEW\_PUB.pep1:\*  
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12: /SIDS5/ptodata/1/pubpaa/US60\_NEW\_PUB.pep1:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	1.0	111	US-10-703-799B-54	Sequence 54, App1
2	7	0.9	64	US-11-087-099-12090	Sequence 12090, A
3	7	0.9	88	US-11-096-568A-5256	Sequence 5256, Ap
4	7	0.9	147	US-11-188-298-3226	Sequence 3226, Ap
5	7	0.9	152	US-11-264-096-2150	Sequence 2150, Ap
6	7	0.9	160	US-11-188-298-13227	Sequence 13227, A
7	7	0.9	174	US-10-873-528-124	Sequence 124, App
8	7	0.9	176	US-11-188-298-8191	Sequence 8191, Ap
9	7	0.9	199	US-11-096-568A-3918	Sequence 3918, Ap
10	7	0.9	206	US-11-232-805-69	Sequence 69, App1
11	7	0.9	225	US-11-096-568A-6604	Sequence 6604, Ap
12	7	0.9	291	US-11-045-004-462	Sequence 462, App
13	7	0.9	302	US-11-188-298-2559	Sequence 2559, Ap
14	7	0.9	302	US-11-188-298-6674	Sequence 6674, Ap
15	7	0.9	316	US-10-196-749-54	Sequence 54, App1
16	7	0.9	316	US-10-194-487-54	Sequence 54, App1
17	7	0.9	316	US-10-195-883-54	Sequence 54, App1
18	7	0.9	316	US-10-195-888-54	Sequence 54, App1
19	7	0.9	316	US-10-195-889-54	Sequence 137, App
20	7	0.9	316	US-10-216-161A-137	Sequence 4, App1
21	7	0.9	316	US-11-152-811-4	

22	7	0.9	316	US-11-264-096-2152	Sequence 2152, Ap
23	7	0.9	318	US-11-194-246-294	Sequence 294, App
24	7	0.9	320	US-11-096-568A-3789	Sequence 3789, Ap
25	7	0.9	420	US-11-074-176-48	Sequence 48, App1
26	7	0.9	426	US-11-188-298-8092	Sequence 8092, Ap
27	7	0.9	426	US-11-188-298-20698	Sequence 20698, A
28	7	0.9	437	US-10-204-639-61	Sequence 61, App1
29	7	0.9	458	US-11-232-805-46	Sequence 46, App1
30	7	0.9	462	US-11-232-805-44	Sequence 44, App1
31	7	0.9	476	US-11-188-298-7595	Sequence 7595, Ap
32	7	0.9	489	US-10-491-468-79	Sequence 29, App1
33	7	0.9	492	US-10-491-468-34	Sequence 34, App1
34	7	0.9	516	US-11-096-568A-27157	Sequence 27157, A
35	7	0.9	519	US-11-096-568A-27156	Sequence 27156, A
36	7	0.9	546	US-10-661-966-18	Sequence 18, App1
37	7	0.9	563	US-11-087-099-4536	Sequence 4536, Ap
38	7	0.9	568	US-11-096-568A-27155	Sequence 27155, A
39	7	0.9	578	US-11-087-099-5335	Sequence 5335, Ap
40	7	0.9	599	US-11-188-298-15409	Sequence 15409, A
41	7	0.9	602	US-10-493-909-51	Sequence 51, App1
42	7	0.9	638	US-11-052-554A-116	Sequence 116, App
43	7	0.9	643	US-11-087-099-5526	Sequence 5526, Ap
44	7	0.9	648	US-11-087-099-6188	Sequence 6188, Ap
45	7	0.9	651	US-11-052-554A-111	Sequence 111, App

#### ALIGNMENTS

RESULT 1  
US-10-703-799B-54  
Sequence 54, Application US/10703799B  
Publication No. US2006078884A1  
GENERAL INFORMATION:  
APPLICANT: Pompeius, Markus  
APPLICANT: Krieger, Burkhard  
APPLICANT: Schroder, Hartwig  
APPLICANT: Zelder, Oskar  
APPLICANT: Haberhauser, Gregor  
APPLICANT: Lee, Heung-Shick  
TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,  
FILE REFERENCE: BGI-124CPN  
CURRENT APPLICATION NUMBER: US/10/703,799B  
CURRENT FILING DATE: 2003-11-07  
PRIOR APPLICATION NUMBER: 09/603,208  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: 60/141031  
PRIOR FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: 60/142692  
PRIOR FILING DATE: 1999-07-01  
PRIOR APPLICATION NUMBER: 60/151214  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: DE 19930429.7  
PRIOR FILING DATE: 1999-07-01  
PRIOR APPLICATION NUMBER: DE 19931413.6  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19931457.8  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19931541.8  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19932209.0  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932230.9  
PRIOR FILING DATE: 1999-07-09  
Number of Prior Application data removed - See File Wrapper or PALM.  
SEQ ID NO 54  
LENGTH: 111  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-10-703-799B-54

Query Match 1.0%; Score 8; DB 9; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 4.1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 FLIVLNL 280  
 |||||  
 DB 86 FLIVLTAL 93

## RESULT 2

US-11-087-099-12090  
 ; Sequence 12090, Application US/11087099  
 ; Publication No. US20060041961A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abad, Mark S. et al.  
 ; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
 ; FILE REFERENCE: 38-21(53450)B EP  
 ; CURRENT APPLICATION NUMBER: US/11/087,099  
 ; CURRENT FILING DATE: 2005-03-22  
 ; NUMBER OF SEQ ID NOS: 12464  
 ; SEQ ID NO 12090  
 ; LENGTH: 64  
 ; TYPE: PRT  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1)..(64)  
 ; OTHER INFORMATION: unsure at all Xaa locations  
 US-11-087-099-12090

Query Match 0.9%; Score 7; DB 11; Length 64;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 ELTELAK 216  
 |||||  
 DB 57 ELTELAK 63

## RESULT 3

US-11-096-568A-5256  
 ; Sequence 5256, Application US/11096568A  
 ; Publication No. US20060048240A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alexandrov, Nikolai et al.  
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
 ; FILE REFERENCE: 2750-1592PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/096,568A  
 ; CURRENT FILING DATE: 2005-04-01  
 ; NUMBER OF SEQ ID NOS: 34471  
 ; SEQ ID NO 5256  
 ; LENGTH: 88  
 ; TYPE: PRT  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)..(88)  
 ; OTHER INFORMATION: Ceres Seq. ID no. 14307700  
 US-11-096-568A-5256

Query Match 0.9%; Score 7; DB 11; Length 88;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 EAKGYA 355  
 |||||  
 DB 12 EAKGYA 18

## RESULT 4

US-11-188-298-3226

; Sequence 3226, Application US/11188298  
 ; Publication No. US20060075522A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abad, Mark S. et al.  
 ; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
 ; FILE REFERENCE: 38-21(53452)B  
 ; CURRENT APPLICATION NUMBER: US/11/188,298  
 ; CURRENT FILING DATE: 2005-07-22  
 ; PRIOR APPLICATION NUMBER: 60/592,978  
 ; PRIOR FILING DATE: 2004-07-31  
 ; NUMBER OF SEQ ID NOS: 22569  
 ; SEQ ID NO 3226  
 ; LENGTH: 147  
 ; TYPE: PRT  
 ; ORGANISM: Glycine max  
 US-11-188-298-3226

Query Match 0.9%; Score 7; DB 11; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 757 TTTTNT 763  
 |||||  
 DB 27 TTTTNT 33

## RESULT 5

US-11-264-096-2150  
 ; Sequence 2150, Application US/11264096  
 ; Publication No. US20060084794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Albumin Fusion Proteins  
 ; FILE REFERENCE: PF546D1  
 ; CURRENT APPLICATION NUMBER: US/11/264,096  
 ; CURRENT FILING DATE: 2005-11-02  
 ; PRIOR APPLICATION NUMBER: 09/833,245  
 ; PRIOR FILING DATE: 2001-04-12  
 ; PRIOR APPLICATION NUMBER: 60/229,358  
 ; PRIOR FILING DATE: 2000-04-12  
 ; PRIOR APPLICATION NUMBER: 60/256,931  
 ; PRIOR FILING DATE: 2000-12-21  
 ; PRIOR APPLICATION NUMBER: 60/199,384  
 ; PRIOR FILING DATE: 2000-04-25  
 ; NUMBER OF SEQ ID NOS: 2267  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2150  
 ; LENGTH: 152  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-264-096-2150

Query Match 0.9%; Score 7; DB 11; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 58;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 DLLAQN 79  
 |||||  
 DB 89 DLLAQN 95

## RESULT 6

US-11-188-298-13227  
 ; Sequence 13227, Application US/11188298  
 ; Publication No. US20060075522A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abad, Mark S. et al.  
 ; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
 ; FILE REFERENCE: 38-21(53452)B  
 ; CURRENT APPLICATION NUMBER: US/11/188,298  
 ; CURRENT FILING DATE: 2005-07-22  
 ; PRIOR APPLICATION NUMBER: 60/592,978  
 ; PRIOR FILING DATE: 2004-07-31





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/ GENERAL INFORMATION:
/ APPLICANT: Alexandrov, Nikolai et al.
/ TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
/ FILE REFERENCE: 2750-1592PUS2
/ CURRENT APPLICATION NUMBER: US/11/096,568A
/ NUMBER OF SEQ ID NOS: 34471
/ SEQ ID NO 6604
/ LENGTH: 225
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ NAME/KEY: misc. feature
/ LOCATION: (1)..(225)
/ OTHER INFORMATION: Ceres Seq. ID no. 14315939
US-11-096-568A-6604

Query Match
Best Local Similarity 100.0%; Score 7; DB 11; Length 225;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 EKFEALT 186
DB 176 EKFEALT 182

RESULT 12
US-11-045-004-462
/ Sequence 462, Application US/11045004
/ Publication No. US20060078901A1
/ GENERAL INFORMATION:
/ APPLICANT: BUCHRIEGER, CARMEN
/ APPLICANT: FRANGEUL, LIONEL
/ APPLICANT: COUVE, ELISABETH
/ APPLICANT: RUSNICK, CHRISTOPHE
/ APPLICANT: FSIHI, HAFIDA
/ APPLICANT: DEHOUX, PIERRE
/ APPLICANT: DUSSEURGET, OLIVIER
/ APPLICANT: CHETOUANI, FARID
/ APPLICANT: MEDJARI, HAFED
/ APPLICANT: GLASER, PHILIPPE
/ APPLICANT: KUNST, FRANK
/ APPLICANT: COSSART, PASCALE
/ APPLICANT: DANIELS, JUSTIN
/ APPLICANT: GOEBEL, WERNER
/ APPLICANT: KREFT, JURGEN
/ APPLICANT: KUHN, MICHAEL
/ APPLICANT: NG, EVA
/ APPLICANT: VAZQUEZ-BOLAND, ANTONIO
/ APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
/ APPLICANT: GARRIDO-GARCIA, PATRICIA
/ APPLICANT: TIERREZ-MARTINEZ, ALBERTO
/ APPLICANT: AMEND, ALEXANDRA
/ APPLICANT: CHAKRABORTY, TRINAD
/ APPLICANT: DOMANN, EUGEN
/ APPLICANT: HAIN, THORSTEN
/ APPLICANT: BERCHE, PATRICK
/ APPLICANT: CHARBIT, ALAIN
/ APPLICANT: DURANT, LIONEL
/ APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
/ APPLICANT: BAQUERO, FERNANDO
/ APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
/ APPLICANT: GOMEZ-LOPEZ, NURIA
/ APPLICANT: MADUENIO, ENCARNIA
/ APPLICANT: PABLOS, BETRIZ DE
/ APPLICANT: WEHLAND, JURGEN
/ APPLICANT: KARST, UWE
/ APPLICANT: ENTIAN, KARL-DIETER
/ APPLICANT: HAUF, JORG
/ APPLICANT: ROSE, MATTHIAS
/ APPLICANT: VOSS, HAMUT
/ TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
```

```
/ FILE REFERENCE: 05394.0018-02
/ CURRENT APPLICATION NUMBER: US/11/045,004
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: 10/637,657
/ PRIOR FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: 10/257,023
/ PRIOR FILING DATE: 2002-10-08
/ PRIOR APPLICATION NUMBER: PCT/FR01/01118
/ PRIOR FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: FR 00/04,629
/ PRIOR FILING DATE: 2000-04-11
/ NUMBER OF SEQ ID NOS: 2854
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 462
/ LENGTH: 291
/ TYPE: PRT
/ ORGANISM: Listeria monocytogenes
US-11-045-004-462

Query Match
Best Local Similarity 100.0%; Score 7; DB 11; Length 291;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 LSKOLKE 147
DB 32 LSKOLKE 38

RESULT 13
US-11-188-298-2559
/ Sequence 2559, Application US/11188298
/ Publication No. US20060075522A1
/ GENERAL INFORMATION:
/ APPLICANT: Abad, Mark S. et al.
/ TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
/ FILE REFERENCE: 38-21(53452)B
/ CURRENT FILING DATE: 2005-07-22
/ PRIOR APPLICATION NUMBER: US/11/188,298
/ PRIOR FILING DATE: 2004-07-31
/ NUMBER OF SEQ ID NOS: 22569
/ SEQ ID NO 2559
/ LENGTH: 302
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa PA01
US-11-188-298-2559

Query Match
Best Local Similarity 100.0%; Score 7; DB 11; Length 302;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 QOLNLEI 60
DB 2 QOLNLEI 8

RESULT 14
US-11-188-298-6674
/ Sequence 6674, Application US/11188298
/ Publication No. US20060075522A1
/ GENERAL INFORMATION:
/ APPLICANT: Abad, Mark S. et al.
/ TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
/ FILE REFERENCE: 38-21(53452)B
/ CURRENT FILING DATE: 2005-07-22
/ PRIOR APPLICATION NUMBER: US/11/188,298
/ PRIOR FILING DATE: 2004-07-31
/ NUMBER OF SEQ ID NOS: 22569
/ SEQ ID NO 6674
/ LENGTH: 302
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa UCBPP-PA14
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US-11-188-298-6674

## Query Match

Best Local Similarity 100.0%; Score 7; DB 11; Length 302;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 QQLNEI 60

Db 2 QQLNEI 8

Search completed: May 15, 2006, 21:00:48  
Job time : 31 secs

## RESULT 15

US-10-196-749-54

; Sequence 54, Application US/10196749

; Publication No. US2006094864A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430R1C340

; CURRENT APPLICATION NUMBER: US/10/196,749

; PRIOR FILING DATE: 2002-07-16

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 54

; LENGTH: 316

; TYPE: PRT

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 233

; OTHER INFORMATION: unknown amino acid

US-10-196-749-54

Query Match 0.9%; Score 7; DB 8; Length 316;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 DILAQGN 79

Db 98 DILAQGN 104

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